

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Bryce Tedeschi Examiner #: 78150 Date: 1/27/01
 Art Unit: 1642 Phone Number 308-4823 Serial Number: 091389545
 Mail Box and Bldg/Room Location: CM1/9TH Floor, room Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Composition and Methods for the prevention & treatment of...

Inventors (please provide full names): Culin R. Dunstan

Earliest Priority Filing Date: 9/3/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

① Amino Acid Residues 186-401 in SEQ. ID #2

② Amino Acid Residues 22-194 in SEQ. ID #2

BEST AVAILABLE COPY

 SE ONLY

Type of Search

Vendors and cost where applicable

Location: <u>308-4499</u>	NA Sequence (#) _____	CTN _____
Searcher Picked Up: _____	AA Sequence (#) _____	Dialog _____
Completed: <u>1/27/01</u>	Structure (#) _____	Questel/Orbit _____
Searcher Prep & Review Time: _____	Bibliographic _____	Dr.Link _____
Clerical Prep Time: _____	Litigation _____	Lexis/Nexis _____
Online Time: _____	Fulltext _____	Sequence Systems _____
	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:24:32 ; Search time 41.41 Seconds

(without alignments)
489.664 Million cell updates/sec

Title: US-09-389-545-2_COPY_22_194
Perfect score: 993
Sequence: 1 ERLPKYLIHNDPETHQLLC.....QKGNATHDNYCSGNREATOR 173

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_fodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	993	100.0	401	11 008712	008712 mus musculu
2	936	94.3	401	11 008727	008727 rattus norv
3	887	89.3	372	4 Q90HP4	Q90HP4 homo sapien
4	887	89.3	401	4 000300	000300 homo sapien
5	420	42.3	300	4 095407	095407 homo sapien
6	390.5	39.3	302	13 Q9PUS0	Q9PUS0 salvelinus
7	300	30.2	459	11 062327	062327 mus musculu
8	298	30.0	439	4 Q16042	Q16042 homo sapien
9	287.5	28.0	482	11 088734	088734 mus musculu
10	278	28.0	655	4 Q75509	Q75509 homo sapien
11	243.5	24.1	616	4 Q9Y606	Q9Y606 homo sapien
12	239	24.1	625	11 035305	035305 mus musculu
13	210.5	21.2	348	12 057112	057112 variola vir
14	210.5	21.2	348	12 085407	085407 variola vir
15	209.5	21.1	349	12 057110	057110 variola vir
16	209.5	21.1	349	12 057111	057111 variola vir
17	209.5	21.1	349	12 089098	089098 variola vir
18	208.5	21.0	349	12 057099	057099 monkeypox v
19	208.5	21.0	349	12 Q89118	Q89118 variola vir

20	208	20.9	349	12 057284	057284 monkeypox v
21	208	20.9	349	12 057098	057098 monkeypox v
22	206.5	20.8	349	12 057281	057281 monkeypox v
23	206.5	20.8	349	12 057100	057100 monkeypox v
24	206.5	20.8	349	12 057101	057101 monkeypox v
25	206.5	20.8	349	12 057102	057102 monkeypox v
26	204	20.5	283	4 Q92956	Q92956 homo sapien
27	204	20.5	283	4 Q9UM65	Q9UM65 homo sapien
28	204	20.5	349	12 057097	057097 monkeypox v
29	203	20.4	348	12 057277	057277 monkeypox v
30	203	20.4	348	12 057103	057103 monkeypox v
31	203	20.4	348	12 057108	057108 monkeypox v
32	202.5	20.4	349	12 057109	057109 variola vir
33	202.5	20.4	350	12 057116	057116 monkeypox v
34	202	20.3	355	12 085308	085308 monkeypox v
35	201.5	20.3	316	12 057092	057092 monkeypox v
36	201	20.2	320	12 057091	057091 monkeypox v
37	201	20.2	320	12 057300	057300 monkeypox v
38	200	20.1	349	12 057305	057305 monkeypox v
39	197	19.8	360	12 057118	057118 monkeypox v
40	196	19.7	351	12 057117	057117 monkeypox v
41	195.5	19.7	326	12 057120	057120 monkeypox v
42	195.5	19.7	326	12 057122	057122 monkeypox v
43	194	19.5	350	12 057123	057123 monkeypox v
44	193.5	19.5	320	12 057079	057079 monkeypox v
45	193.5	19.5	351	12 073559	073559 monkeypox v

ALIGNMENTS

RESULT 1
ID 008712 PRELIMINARY; PRT: 401 AA.
AC 008712; 070202;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE OSTEOCLASTOGENESIS INHIBITORY FACTOR.
DE (OCIF).
GN TNFRSF11B OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shuman
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patl,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density.";
RT Cell 89:309-319(1997).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola. AND NIH SWISS;
RX MEDLINE=96382527; PubMed=9714833;
RA Higashio K.,
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morin J.P.,
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OPG)
RT gene and its expression in embryogenesis.";
RL Gene 215:339-343(1998).
-I- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF BONE
SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING PATHWAYS
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
-I- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94331; AAB53708.1; -.
 DR EMBL: AB013898; BAA28269.1; -.
 DR EMBL: AB013903; BAA33388.1; -.
 DR EMBL: AB013899; BAA33388.1; JOINED.
 DR EMBL: AB013900; BAA33388.1; JOINED.
 DR EMBL: AB013901; BAA33388.1; JOINED.
 DR EMBL: AB013902; BAA33388.1; JOINED.
 DR HSSP: P25942; ICDF.
 DR MGD: MG1:109587; Opg.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50017; DEATH DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 DR Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 23 63 TNFR-CYS 2.
 FT REPEAT 64 106 TNFR-CYS 3.
 FT REPEAT 107 143 TNFR-CYS 4.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH SWISS).
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH SWISS).
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 100.0%; Score 993; DB 11; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.7e-96;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETLPPKYLHVPETGHOILCDKCAPGYTLKOHCTVRRKTLCPDPHSYDSDSWHTSDECV 60
 DB 22 ETLPPKYLHVPETGHOILCDKCAPGYTLKOHCTVRRKTLCPDPHSYDSDSWHTSDECV 81
 QY 61 YCSFVCKELOSVOKEOENRHNRCVCEGEGRYLEIEFCLKHSRCPGSGGVVQAGTPERNV 120
 DB 82 YCSFVCKELOSVOKEOENRHNRCVCEGEGRYLEIEFCLKHSRCPGSGGVVQAGTPERNV 141
 QY 121 CKKCPDFFSGEETSSKAPCIKHTNCSFFGLLLLOKGNATHNVCSSGRRERATK 173
 DB 142 CKKCPDFFSGEETSSKAPCIKHTNCSFFGLLLLOKGNATHNVCSSGRRERATK 194

RESULT 2
 ID 008727 PRELIMINARY; PRT; 401 AA.
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OSIF).
 OS TNFRSF11B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamura J.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trill G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derdy P., Lee R.,
 RA Sugis S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 of bone density.";
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF HEAVILY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REG.
 DR EMBL: U94330; AAB53707.1; -.
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1.
 DR Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;

Query Match 94.3%; Score 936; DB 11; Length 401;
 Best Local Similarity 93.6%; Pred. No. 3.4e-90;
 Matches 161; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 ETLPPKYLHVPETGHOILCDKCAPGYTLKOHCTVRRKTLCPDPHSYDSDSWHTSDECV 60
 DB 22 ETLPPKYLHVPETGHOILCDKCAPGYTLKOHCTVRRKTLCPDPHSYDSDSWHTSDECV 81
 QY 61 YCSFVCKELOSVOKEOENRHNRCVCEGEGRYLEIEFCLKHSRCPGSGGVVQAGTPERNV 120
 DB 82 YCSFVCKELOSVOKEOENRHNRCVCEGEGRYLEIEFCLKHSRCPGSGGVVQAGTPERNV 141
 QY 121 CKKCPDFFSGEETSSKAPCIKHTNCSFFGLLLLOKGNATHNVCSSGRRERATK 173
 DB 142 CKKCPDFFSGEETSSKAPCIKHTNCSFFGLLLLOKGNATHNVCSSGRRERATK 194

Db 22 ETPPKYLYHDEBTGHCGLDCKCAPGTYLKOHCTVRRKTLVCVPCDPYSTDSMHTSDECV 81
 QY 61 YCSPVCKELQSVKQECNRTNHNRYCECEGRYLEIEFCLHRSRCPSSGVVQAGTPERNIV 120
 Db 82 YCSPVCKELQTVKQECNRTNHNRYCECEGRYLEIEFCLHRSRCPGLGVQAGTPERNIV 141
 QY 121 CKKCPDGFSSGTSKAPCIKHTNCSFTGLLLIÖKGNATHDVCSGNREATQ 172
 Db 142 CKKCPDGFSSGTSKAPCIKHTNCSFTGLLLIÖKGNATHDVCSGNREATQ 193

RESULT 3
 Q9UHP4 PRELIMINARY: PRT: 372 AA.

Q9UHP4: 01-MAY-2000 (TREMBLREL. 13, Created)
 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
 01-OCT-2000 (TREMBLREL. 15, Last annotation update)
 OSTROPROTEGERIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens."
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
 DR EMBL: AF134187; AAF20168.1;
 DR HSSP: P25942; 1CDF.
 DR INTERPRO: IPR001368;
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 FT SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 89.3%; Score 887; DB 4; Length 372;
 Best Local Similarity 87.3%; Pred. No. 4.3e-85;
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

1 ETPPKYLYHDEBTGHCGLDCKCAPGTYLKOHCTVRRKTLVCVPCDPYSTDSMHTSDECV 60
 1 ETPPKYLYHDEBTGHCGLDCKCAPGTYLKOHCTVRRKTLVCVPCDPYSTDSMHTSDECV 60
 Db 1 ETPPKYLYHDEBTGHCGLDCKCAPGTYLKOHCTVRRKTLVCVPCDPYSTDSMHTSDECV 60
 QY 61 YCSPVCKELQSVKQECNRTNHNRYCECEGRYLEIEFCLHRSRCPSSGVVQAGTPERNIV 120
 Db 61 YCSPVCKELQSVKQECNRTNHNRYCECEGRYLEIEFCLHRSRCPSSGVVQAGTPERNIV 120
 QY 121 CKKCPDGFSSGTSKAPCIKHTNCSFTGLLLIÖKGNATHDVCSGNREATQ 173
 Db 121 CKKCPDGFSSGTSKAPCIKHTNCSFTGLLLIÖKGNATHDVCSGNREATQ 173

RESULT 4
 Q000300 PRELIMINARY: PRT: 401 AA.

Q000300: 060236;
 01-JUL-1997 (TREMBLREL. 04, Created)
 01-JUL-1997 (TREMBLREL. 04, Last sequence update)
 01-OCT-2000 (TREMBLREL. 15, Last annotation update)
 OSTROPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;

RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.S.,
 RA Luehry R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 of bone density."
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG FIBROBLAST;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 osteoclastogenesis in vitro."
 RL Endocrinology 139:1329-1337(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE=98351569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 osteoprotegerin/osteoclastogenesis-inhibitory factor."
 RL Eur. J. Biochem. 254:685-691(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
 KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
 A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
 THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB002146; BAA25910.1;
 DR EMBL: AB008822; BAA32076.1;
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1;
 DR HSSP: P25942; 1CDF.
 DR MIM: 602643;
 DR INTERPRO: IPR001368;
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -1.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1
 FT CHAIN 21
 FT DOMAIN 22 401
 FT REPEAT 23 183
 FT REPEAT 24 63
 FT REPEAT 25 106
 FT REPEAT 26 107
 FT REPEAT 27 143
 FT REPEAT 28 144
 FT REPEAT 29 201
 FT DOMAIN 306 365
 FT DISULFD 41 54
 FT DISULFD 42 62
 FT DISULFD 43 97
 FT DISULFD 44 83
 FT DISULFD 45 105
 FT DISULFD 46 142
 FT DISULFD 47 148
 FT DISULFD 48 160
 FT CARBOHYD 49 98
 FT CARBOHYD 50 152
 FT CARBOHYD 51 165
 FT CARBOHYD 52 178

062327
ID 062327 PRELIMINARY; PRT: 459 AA.
AC 062327:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOB;
RX MEDLINE=95176848; PubMed=7873884;
POVELL E.E., WICKER L.S., PETERSON L.B., TODD J.A.;
"Allelic variation of the type 2 tumor necrosis factor receptor
gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL: X76401; CA53981.1; -;
DR HSSP: P19438; INCF.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
FT NON_TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 30.2%; Score 300; DB 11; Length 459;
Best Local Similarity 35.2%; Pred. No. 1,4e-23;
Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;

OY 10 YDPETHG-----QILCDKCAPGYTLKQHCYRRKTLCPVPCDHSYTDSSMHTS 56
DB 17 YKPEPGYECQISOEYDRKRAQMCCKCPGGYVKKHCKNTSDTVACDCASMYTVMNQF 76
OY 57 DECVYSPCKELQSVKQECNRTNHRVCECEBGRYLEIF-----CLKHSCPPGSGV 109
DB 77 RTCLSCSSSCSTQDYETRACTKQONRVCACEAGRYCALKTHSGRCQCRKLSKCGRGV 136
OY 110 VQAGPERNTVCKCPDGFSGETSSKAPCIKHTNCSTFGILLIQGNATHDNVCS 165
DB 137 ASSRAPNGVILCKACAPGTFSTSTVDCRPFRICS---ILAIIPGNASTDAVCA 188
RESULT 8
ID 016042 PRELIMINARY; PRT: 439 AA.
AC 016042:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
Brockhaus M., Leschler W.;
"Two human TNF receptors have similar extracellular, but distinct
intracellular, domain sequences.";
RL Cytochrome 2:231-237(1990).
DR EMBL: S63368; AAB19824.1; -;
DR HSSP: P25942; ICDF.

DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PRODOM: PD000771; -; 1.
SQ SEQUENCE 439 AA; 46090 MW; FBECBE329C67FF6 CRC64;

Query Match 30.0%; Score 298; DB 4; Length 439;
Best Local Similarity 35.6%; Pred. No. 2.2e-23;
Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;

OY 10 YDPETHG-----QILCDKCAPGYTLKQHCYRRKTLCPVPCDHSYTDSSMHTS 57
DB 10 YKPEPGYECQISOEYDRKRAQMCCKCPGGYVKKHCKNTSDTVACDCASMYTVMNQF 69
OY 58 DECVYSPCKELQSVKQECNRTNHRVCECEBGRYLEIF-----EFLKHSPPGSGV 111
DB 70 ECLSCGSSSDQVETQACTREONNRCRPGWYCALSKQEGCRCLARCRGPGVVA 179
OY 112 AGTPERNTVCKCPDGFSGETSSKAPCIKHTNCSTFGILLIQGNATHDNVCS 165
DB 130 PETERSDVYCKCAPGTFSTSTVDCRPFRICS---ILAIIPGNASTDAVCA 174

RESULT 9

ID 088734 PRELIMINARY; PRT: 482 AA.

AC 088734:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE P80 TNF-ALPHA RECEPTOR.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hurtle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
"The Mouse Tumor Necrosis Factor Receptor Gene: Genomic Structure,
RT Characterization of the two Transcripts.";
RL Genomics 0:0-0(0).

DR EMBL: Y14619; CAAT74969.1; -;
DR EMBL: Y14620; CAAT74969.1; JOINED.
DR EMBL: Y14621; CAAT74969.1; JOINED.
DR EMBL: Y14622; CAAT74969.1; JOINED.
DR EMBL: Y14623; CAAT74969.1; JOINED.
DR EMBL: Y14679; CAAT74969.1; JOINED.
DR HSSP: P19438; INCF.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PRODOM: PD000771; -; 1.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 29.0%; Score 287.5; DB 11; Length 482;
Best Local Similarity 33.9%; Pred. No. 3.1e-22;
Matches 62; Conservative 17; Mismatches 73; Indels 31; Gaps 4;

OY 10 YDPETHG-----QILCDKCAPGYTLKQHCYRRKTLCPVPCDHSYTDSSMHTS 57
DB 32 YKPEPGYECQISOEYDRKRAQMCCKCPGGYVKKHCKNTSDTVACDCASMYTVMNQF 91
OY 50 TDSWHTDECVYSPCKELQSVKQECNRTNHRVCECEBGRYLEIF-----CLKHSCPPGSGV 102
DB 92 TQVWNPFTCLSCSSSCSTQDYETRACTKQONRVCACEAGRYCALKTHSGRCQCRKLSK 151
OY 103 CPPGSGVYVQAGTPERNTVCKCPDGFSGETSSKAPCIKHTNCSTFGILLIQGNATHDNVCS 162

ID	Y	163	VCS	165
Db	152	CGPGCVASSRBPANGNVILKACACPGTFSDTTSSPDVCRPHAFICS----	IIAIPGNASTDA	207
Y	11:	208	VCA	210
RESULT 10				
075509				
ID	075509	PRELIMINARY:	PRT:	655 AA.
AC	075509:			
DT	01-NOV-1998	(TREMblrel. 08, Created)		
DT	01-NOV-1998	(TREMblrel. 08, Last sequence update)		
DT	01-OCT-2000	(TREMblrel. 15, Last annotation update)		
DE	TNFR-RELATED DEATH RECEPTOR-6 (DJ18J13.1) (DR6 OR DJ18J13.1. RECEPTOR-6)).			
GN	DR6 OR DJ18J13.1.			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,			
RL	Vincent C., Aggarwal B.B., Dixit V.M.,			
RT	Identification and functional characterization of DR6, a novel death			
RL	domain-containing TNF receptor.			
RN	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.			
RP	[2]			
RA	SEQUENCE FROM N.A.			
RL	Parker A.,			
DR	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF068868; AAC34583.1; -.			
DR	EMBL: AL096801; CAB75692.1; -.			
DR	HSSP: P07174; INGR.			
DR	INTERPRO: IPR000488; -.			
DR	INTERPRO: IPR001368; -.			
DR	PFAM: PF00020; TNFR_c6; 4.			
DR	PFAM: PF00531; death; 1.			
DR	PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.			
DR	PROSITE: PS50017; DEATH_DOMAIN; 1.			
DR	PROSITE: PS50050; TNFR_NGFR_2; 1.			
DR	PRODOM: PD000771; -; 1.			
KW	Receptor.			
SO	SEQUENCE	655 AA;	71844 MW;	48939391C4852A33 CRC64;
Query Match		28 0%;	Score 278;	DB 4; Length 655;
Best Local Similarity		36.18;	Pred. No. 4.1e-21;	
Matches	57;	Conservative	19;	Mismatches 82; Indels 0; Gaps
Y	7	YLAHDPETGHOLLDKCAPGTLYLKQHCIVRRKTLTCVPCPPHSTYDWSHTSDECGYSPVC	66	
Y	54	YRHDRATRGQVLTCDKCPAGTYVEHCTNSLRVSCSPGVTFRHNGIEKCHDSQPC	113	
Y	67	KELOSVKQECNRTHNRVCECEGNYLEIEFLCKHRSCPPSGGVQACTPERNRYCKKCPD	126	
Db	114	PWPMIEKILPCALINDRECTCPBGMFOSNATCAPHTVCYGVGAVKKGKGTETEDVRKQCAR	173	
Y	127	GFGSGTSSKAPCIKHTNCSIFGLLLIQKGATHTDNYC	164	
Db	174	GTFSDVDPSSVMKCAKYTDCLSLQNLVLIKPGTKETDNYC	211	
RESULT 11				
09Y606				
ID	09Y606	PRELIMINARY:	PRT:	616 AA.
AC	09Y606:			
DT	01-NOV-1999	(TREMblrel. 12, Created)		
DT	01-NOV-1999	(TREMblrel. 12, Last sequence update)		
DT	01-OCT-2000	(TREMblrel. 15, Last annotation update)		
DE	RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-INDUCED CYTOKINE RECEPTOR) (RANK).			

QY	DB	Match	Similarity	Conservative	Score	DB	Length	Indels	Gaps
QY	20	CDKAPGTYLKHCHVARKRLTCVPCPDHSYDMSMTSCQCYVCSPC--KELQSVKQDC	24.5%	19	243.5	76	616	7	4
DB	47	CNKCEPGKTYMSKCTTTSVDSVCLPGCPREYLDLSMNEEDCL-LHKVYCDTGKALVAVN..	35.3%	19	1.6e-17	104	616	7	4
QY	77	NRTNHRVCECEBGRY--LEIEFCLKHSRCPSGSGVGAQTPRENTVCKKCPDGFPSGET	24.5%	19	243.5	134	616	7	4
DB	105	NSTPRRACAGIAGYMSDDCECCRNTECAPGLGQNHQLQINKDVKRCPLAGYFSDAHS	35.3%	19	1.6e-17	164	616	7	4
QY	135	SKAPCIKHTNCSFEGLLILQKGNATHDVNCSGNREA	24.5%	19	243.5	170	616	7	4
DB	165	STDKCRPWTNCTFLGKRVENHGTESKDVAVSSSLPA	35.3%	19	1.6e-17	200	616	7	4

AC		035305;	(Tremblrel_05, Created)
AD	01-JAN-1998	(Tremblrel_05,	Last sequence update)
AE	01-JAN-1998	(Tremblrel_05,	Last sequence update)
AF	01-OCT-2000	(Tremblrel_15,	Last annotation update)
AG	RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-		
AH	INDUCED CYTOKINE RECEPTOR) (RANK).		
AI	TNFRSF1A OR RANK.		
AJ	Mus musculus (Mouse).		
AK	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		
AL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AM	NCHI_TaxID=10090;		
AN	[1]		
AO	SEQUENCE FROM N.A.		
AP	TISSUE=LIVER EPITHELIUM:		
AQ	MEDLINE=96032977; PubMed=93671155;		
AR	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,		
AS	Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,		
AT	Gallibert L.;		
AV	"A homologue of the TNF receptor and its ligand enhance T-cell growth		
AW	and dendritic-cell function.";		
AX	Nature 390:175-179(1997).		
AY	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.		
AZ	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).		
BA	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.		
BB	EMBL: AF019046; AAB86810.1; -.		
BC	HSSP: P25642; ICDF.		
BD	MCD; MG1:J314891; Trnfsfla.		
BE	INTERPRO: IPRO00561; -.		
BF	INTERPRO: IPRO01368; -.		
BG	Pfam: PF00020; TNFR_c6; 3.		
BH	DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.		
BI	DR PROSITE: PS01186; EGF_2; UNKNOWN_1.		
BJ	DR PROSITE: PS00050; TNFR_NGFR_2; 1.		
BK	DR PRODOM: PD000771; -; 1.		
BL	KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.		
BM	FT SIGNAL	1	30
BN	FT CHAIN	31	625
BO	FT DOMAIN	31	214
BP	FT TRANSMBM	215	235
BQ	FT DOMAIN	236	625
BR	FT REPEAT	34	196
BS	FT REPEAT	34	70
BT	FT REPEAT	71	114
BU	FT REPEAT	115	153
BV	FT REPEAT	154	196
BW	FT DISULFD	35	47
BX	FT DISULFD	48	61
BY	FT DISULFD	51	69
BZ	FT DISULFD	72	87
CA	FT DISULFD	93	113
CB	FT DISULFD	115	125
CC	FT DISULFD	127	134
CD	FT DISULFD	128	152
CE	FT DISULFD	156	170
CF	FT DISULFD	175	195
CG	FT CARBOHYD	106	106
CH	FT CARBOHYD	175	175
CI	SEQUENCE	625 AA;	66621 MM;
CJ		F8C81872E99511DBE CRC64;	(POTENTIAL).

	Query Match Similarity	24.1%	Score 239;	DB 11	Length 625;
	Best Local Smilarity	33.9%	Pred. No. 4,7e-17;		
	Matches	59;	Conservative	21;	Mismatches 82; Indels 12; Gaps 7
Oy	1	ETLPAP-KYLHNPETGHOILCDKCAPGYVLQONCHTRRRKTLCPSPDHSYDSMTSDE	58		
		: : : : : : : : : : : : : : : : : : : :			
Dd	30	QVTPPTCGERHNE-HLGR--CCSRCEPKYLLSKCPIPTSDSVCLPCGPREDYLDITWMEEDK	86		
		: : : : : : : : : : : : : : : : : : : :			
Oy	59	CVYCSPVC---KEIISVKOEENRTHNRVCECEGRAY-LIEIFCLKHRSCPPSGGVYAG	113		
		: : : : : : : : : : : : : : : : : : : :			
Dd	87	CL-LHKVCDAGAKALVAIV-DPGNHHTAPRRACATAGAYHMNSDCDECRCRNTECAPOFGAQNPL	144		
		: : : : : : : : : : : : : : : : : : : :			
Oy -	114	TPERNTVCKCKCPDGCFEGSGTSSKAPCIKTNTSTFGLLILOKNATHDNVCSGN	167		

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Db      145  QLNKDTVCTPCLLTGFFSDVFSSTDKCKXPMTNCTLLGKLEAHQGTSTEDSVVCCSS 196
RESULT  13
057112  ID
057112  PRELIMINARY; PRT; 348 AA.
AC      057112
057112:
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN      CRMB.
OS      Variola virus.
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae.
OX      Orthopoxvirus.
NC      NCBI_TaxID=10255;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN='WHITEPOX' CHIMP 9-2 (CH9-2);
RA      Loparev V.N., Parsons J.M., Esposto J.J.;
RL      Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RR      EMBL; U08151; AAB94376.1; -.
DR      HSSP; P25942; ICDF.
DR      INTERPRO: IPR001368; -.
DR      PFAM; PF00020; TNFR_C6; 2.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
DR      PROSITE; PS50050; TNFR_NGFR_2; 2.
DR      PRODOM; PD000771; -. 1.
SQ      SEQUENCE 348 AA; 38041 MW; 92D333794FC373E3 CRC64;

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Query Match Similarity      21.2%; Score 210.5; DB 12; Length 348;
Best Local Similarity      30.0%; Pred. No. 2,6e-14;
Matches      48; Conservative      19; Mismatches      76; Indels      17; Gaps      4

Oy      10 YDPETG-----HOLLCDKCAFGTYLKQHCIVARRKTLGVCPDHSYTDMSWHTSDP.V 60
Db      24 YTPPNQCKCKDTEYRKRNHLCCLSCSPGTYVASRLCDSKTNTQCPGSGGTSPNNHLP.V 60
Oy      61 YCSPPCKELQSVKQCCNRTNRHNVCCCEERYLEI-----EFLKLRSPSPSSGVQAQT 114
Db      84 SCNGRCNSNQVETRRSCNTTHNRICCSPEGYLLGLGSSGCKACVQSTQKGIYGV-VSCHPT 142
Oy      115 PERNTVCKKCPDGFPSGSETSKAPCIKHTNCSTFGLLIQ 154
Db      143 SVGDYICSPCGRGTYSHYVSSADKPEPVN-NTFNWIDVE 181

RESULT      14
ID      085407
NC      085407;
DC      PRELIMINARY;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      HOMOLOG OF VACCINIA VIRUS CDS B28R.
GN      G2R OR CRMB.
OS      Variola virus.
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Orthopoxvirus.
OX      NCBI_TaxID=10255;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BANGLADESH-1975;
RX      MEDLINE=94088747; PubMed=8264798;
RA      Massung R.F., Esposito J.J., Liu L.I., Qi J., Uterback T.R.,
RA      Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.;
RT      "Potential virulence determinants in terminal regions of variola
RL      smallpox virus genome.";
RL      Nature 366:748-751(1993).
RP      [2]
RP      SEQUENCE FROM N.A.

```

JC STRAIN='WHITEPOX', CHIMP 9-4 (CH9-4);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases
 DR EMBL; L225257; AAC60933.1; -
 DR EMBL; U08152; AAB94377.1; -
 DR HSP; P25942; ICDF.
 DR INTERPRO: IPR001368;
 DR PFAM: PFD0020; TNFR_c6; 2.
 DR PROSITE: PSS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PSS00650; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -; 1
 SO SEQUENCE 348 AA; 38075 MW; A9BE85AF94AB5365 CMC6;

Db 144 SVGDVICSPCGFGTYSTVSSADKCEPVPN-NTFNYIDVE 182

Search completed: January 27, 2001, 11:24:34
Job time: 116 sec

Query Match	21.28;	Score 210.5;	DB 12;	Length 348;
Best Local Similarity	30.08;	Pred. No. 2.6e-14;		
Matches 48;	Conservative 19;	Mismatches 76;	Indels 17;	Gaps 41;

QY 10 YDPENG-----HOLDCKAPGYULKHCNIVARRKTLCPDRHSYDSDNWTSECV 60

Db 24 YTPNGKCKOTERYKRHNKLCSCSPRGYASLDCSKNTKTCOTPCGSGFTFSRNHNLPACL 83

QY 61 YCSPVCKELOSVCQNCNTHNRVCECEGRLEI-----EFCIKHNSCPRGSGVNOAGT 114

84 SCNGRCSNOVETSCNTHNRICECSPGYCLLKSGSGCKACVSYOTKCGIGYV-SGHT 142

QY 115 PERNTVCKKCPDGFSGSETSKAPCIRKHTKSTFGLLLIQ 154

Db 143 SVGDVICSPCGCGFYSHTVSSADNCEPVN-NTFNNTYDIE 181

RESULT	ID	PRELIMINARY;	PRT;	349 AA.
057110	057110			
AC	057110;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.			
GN	CRMB.			
OS	Varicella virus.			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
OX	NCBI_TaxID=10255;			
UN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MAJOR, CONGO-1970 (CNG-70);			
RA	Loparev V.N., Parsons J.M., Esposito J.J.;			
RL	Submitted (FEB-1997) to the EMBL/Genbank/DBD databases.			
DR	EMBL; U08147; AAB94372.1; -.			
DR	HSSP; P25942; ICDF.			
DR	INTERPRO; IPR001368; -.			
DR	PFAM; PF00020; TNFR_c6; 2.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE; PSS0050; TNFR_NGFR_2; 2.			
DR	PRODOM; PD000771; -; 1.			
SO	SEQUENCE 349 AA; 36273 MW; 2987FE00CD4824F5 CRC64;			

Query Match	21.1%	Pred. 209.5;	DB 12;	Length 349;
Best Local Similarity	30.0%	Pred. No. 3.3e-14;		
Matches 48; Conservative	19;	Mismatches 76;	Indels 17;	Gaps 4;

```

QY 10 YDPEFG-----HOLLDKCAPGYLMOHCIVARKTLCVCPDPRHSYDMSHTSDCY 60
Db 25 YTPNGKCKDTEYKRHNLCCLSCPPGYASRLCSKTNQCTPCGSGTFSRNNHPLACL 84

QY 61 YCSFVCKELOSVCOEKNRTHNRVCECEGRYLEI-----EFLCKHRSCPSPGSGVOAGT 114
Db 85 SCNRCSMNQVETSCMTHNRICECPGYCLLKSSGCKACVSYQKCGIGYG-VSGHT 143

QY 115 PERNTVCCKCPDGFSGSETSKAPCICKHTNCSFTGLLLIQ 154

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:24:56 ; Search time 17.62 Seconds
(without alignments)
317.076 Million cell updates/sec

Title: US-09-389-545-2_COPY_22_194
Perfect score: 993
Sequence: 1 ETLPKRLIHDPEYGHQLJC.....QKGNATHDNYCSGNREATQR 173

String table: BIOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	30.2	461	1	TNFR2_HUMAN
2	297	29.9	474	1	TNFR2_MOUSE
3	270	27.2	289	1	CD40_MOUSE
4	261	26.3	277	1	CD40_HUMAN
5	242.5	24.4	435	1	TNRC_HUMAN
6	227	22.9	269	1	CD40_BOVIN
7	226	22.8	325	1	VT2_SFVKA
8	210.5	21.2	349	1	VT2_MYXVL
9	210.5	21.2	349	1	VT22_VARY
10	203.5	20.5	415	1	TNRC_MOUSE
11	192.5	19.4	427	1	NGFR_HUMAN
12	188.5	19.0	425	1	NGFR_RAT
13	184	18.5	416	1	NGFR_CHICK
14	177	17.8	256	1	41BB_MOUSE
15	167	16.8	255	1	41BB_HUMAN
16	167	16.8	323	1	FASA_BOVIN
17	163	16.4	271	1	OX40_RAT
18	160	16.1	455	1	TNRI_HUMAN
19	159	16.0	454	1	TNRI_MOUSE
20	159	16.0	461	1	TNRI_PIG
21	152	15.3	272	1	OX40_MOUSE
22	148	14.9	461	1	TNRI_RAT
23	145	14.6	277	1	OX40_HUMAN
24	144.5	14.6	332	1	FASA_PIG
25	144	14.5	335	1	FASA_HUMAN
26	139	14.0	595	1	CD30_HUMAN
27	137.5	13.8	324	1	FASA_RAT
28	137	13.8	327	1	FASA_MOUSE
29	135	13.6	471	1	TNRI_BOVIN
30	125	12.6	1680	1	FUR2_DROME
31	118.5	11.9	1609	1	LMG1_HUMAN
32	115	11.6	417	1	WSL1_HUMAN
33	113.5	11.4	260	1	CD27_HUMAN

ALIGNMENTS

34	113.5	11.4	1607	1	LMG1_MOUSE
35	111	11.2	1955	1	ACRI_CHICK
36	109.5	11.0	250	1	CD27_MOUSE
37	109.5	11.0	667	1	TS11_GIALA
38	109	11.0	969	1	PAC4_HUMAN
39	108	10.9	713	1	TS4_GIALA
40	108	10.9	915	1	PAC6_MOUSE
41	107.5	10.8	722	1	DL1_MOUSE
42	107	10.8	1639	1	LMG1_DROME
43	106.5	10.7	3084	1	LM41_MOUSE
44	106	10.7	915	1	PAC6_RAT
45	105	10.6	1557	1	LM1_CAEEL
Q18823					ceenorhadi
P02468					mus musculus
P31696					gallus gall
P41272					mus musculus
Q03185					gallus gall
P29122					homo sapien
P21849					gallus gall
Q04592					mus musculus
Q61483					mus musculus
P15215					discophila
P19137					mus musculus
P41413					rattus norv
Q18823					ceenorhadi
RESULT 1					
TNFR2_HUMAN					
ID TNFR2_HUMAN	STANDARD:	PRT:	461 AA.		
AC P20333:					
DT 01-FEB-1991 (Rel. 17, Created)					
DR 01-AUG-1991 (Rel. 19, Last sequence update)					
DI 01-OCT-2000 (Rel. 40, Last annotation update)					
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFR2) (P80) (TNF-R2) (P75) (CD120B) (ETANERCEPT)					
GN TNFR2_HUMAN					
OS Homo sapiens (Human)					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
LN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=90260639; PubMed=2160731;					
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;					
RA "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";					
RT Science 248:1019-1023(1990).					
RL [2]					
RN SEQUENCE FROM N.A.					
RX MEDLINE=91045991; PubMed=2172983;					
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;					
RA "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";					
RT Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).					
RL [3]					
RN SEQUENCE FROM N.A.					
RX MEDLINE=96299745; PubMed=8661109;					
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S., Lepeslier D., Stallard B.J., Goeddel D.V., Desautave F.J., Brodeur G.M.;					
RA "Physical mapping and genomic structure of the human TNFR2 gene.";					
RT Genomics 35:94-100(1996).					
RL [4]					
RN SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE.					
RX MEDLINE=90349572; PubMed=2166946;					
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;					
RA "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";					
RT Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).					
RL [5]					
RN SEQUENCE OF 27-31.					
RX MEDLINE=90110215; PubMed=2153136;					
RA Engelmann H., Novick D., Wallach D.;					
RA "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";					
RT J. Biol. Chem. 265:1531-1536(1990).					
RL [6]					
RN SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.					
RX MEDLINE=91056048; PubMed=2173696;					

RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from H60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RP CHARACTERIZATION.
 RP MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
 RP MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBEL (IMMUNEX AND
 CC WYETH-AVERT). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBEL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROW; NOTE=CD guide CD120b entry;
 CC WWW=http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"
 CC -1- DATABASE: NAME-Embel; NOTE=Clinical information on Embrel;
 CC WWW=http://www.embelinfo.com/".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M32315; AAA59929.1; -;
 DR EMBL: M35857; AAA63262.1; -;
 DR EMBL: U52165; AAC50622.1; -;
 DR EMBL: U52156; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA36755.1; -;
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MTM: 191191; -;
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_c6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 258 287 POTENTIAL.
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 39 201 4 X TNFR-CYS.
 FT REPEAT 39 201 TNFR-CYS 1.
 FT REPEAT 77 118 TNFR-CYS 2.
 FT REPEAT 119 162 TNFR-CYS 3.
 FT REPEAT 163 201 TNFR-CYS 4.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 R -> P (IN REF. 4).
 FT CONFLICT 141 141 R -> T (IN REF. 1 AND 3).
 FT CONFLICT 196 196 A -> T (IN REF. 4).
 FT CONFLICT 363 363
 SQ SEQUENCE 461 AA; 48316 MM; 603B580CD67636F CRC64;
 Query Match 30.2%; Score 300; DB 1; Length 461;
 Best Local Similarity 35.6%; Pred. No. 5.1e-19;
 Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;
 QY 10 YDPETGH-----QLLDKCAPGTLYLKQCHTRRRLKLCVCPDHSYDWSHTSD 57
 Db 32 YAPRPGSTRLREYDQTQAGMCCSKSPGHAKVFCKTSDYDCSDCEDSTYTQLMWVP 91
 QY 58 ECVYCSVCKELDSVKOECKRTHNRVCECEGRLEI-----EFLKHSCEPGSGVQ 111
 Db 92 ECISGSRCSDDYETQACREONRITCRPGWCAISKQEGRLCAPLRKCRPGGVAR 151
 QY 112 AGPERNTVCKKCPDGFSEGTSSKAPCIRHTNCSFGLLLQGNATHDNVCS 165
 Db 152 PGFETSVCKPCAPGFTSNTSSTDICRPHQICNVAVI-----PGNASKAVCT 201
 RESULT 2
 TNFR2_MOUSE STANDARD; PRT; 474 AA.
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]

RP SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN-NOD:
 RA Jacob C.O., Liu J.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RM [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=LIVER;
 RA Kissonerghis M., Fellows R., Feldmann M., Chernajovsky Y.;
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC -----
 DR EMBL: M60469; AAA39752.1; -
 DR EMBL: M59378; AAA40463.1; -
 DR EMBL: U39488; AAA85021.1; -
 DR EMBL: X87128; CAA60618.1; -
 DR PIR: B38634; B38634.
 DR HSSP: P19438; 1NCF.
 DR MGD: MGI:1314883; TNFRSF1B.
 DR INTERPRO: IPR001368; -
 DR PFAW: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 RA Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 259 288 POTENTIAL.
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 203 4 X TNFR-CYS.
 FT REPEAT 39 77 TNFR-CYS 1.
 FT REPEAT 78 119 TNFR-CYS 2.
 FT REPEAT 120 164 TNFR-CYS 3.
 FT REPEAT 165 203 TNFR-CYS 4.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 29.9%; Score 297; DB 1; Length 474;
 Best Local Similarity 35.2%; Pred. No. 9.5e-19;
 Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;

RESULT 3
 CD40_MOUSE STANDARD; PRT: 289 AA.
 ID CD40_MOUSE
 AC P27512;
 DT 01-AUG-1996 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (M40).
 GN TNFRSF5 OR CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:92105763; PubMed:1370315;
 RA Torres R.M., Clark E.A.;
 RT "Differential increase of an alternatively polyadenylated mRNA species of murine CD40 upon B lymphocyte activation."
 RL J. Immunol. 148:620-626(1992).
 RN [2]
 RP REVISIONS.
 RC STRAIN-BALB/C;
 RA Torres R.M.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RM [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=LIVER;
 RX MEDLINE:93094586; PubMed:1281194;
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A., Howard M., Cockayne D.A.;
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene."
 RL J. Immunol. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
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 CC -----
 DR EMBL: M8312; AAB08705.1; -
 DR EMBL: M94126; AAA37404.1; -
 DR EMBL: M94129; AAA37404.1; JOINED.
 DR EMBL: M94128; AAA37404.1; JOINED.
 DR EMBL: M94127; AAA37404.1; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P25942; 1CDF.
 DR MGD: MGI:88336; TNFRSF5.
 DR INTERPRO: IPR001368; -
 DR PFAW: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 RA Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 289 CD40L RECEPTOR.
 FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 216 289 POTENTIAL.
 FT DOMAIN 25 187 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 25 60 4 X TNFR-CYS.
 FT REPEAT 61 103 TNFR-CYS 1.
 FT REPEAT 104 144 TNFR-CYS 2.
 FT REPEAT 145 187 TNFR-CYS 3.
 FT CARBOHYD 153 153 TNFR-CYS 4.
 SO SEQUENCE 289 AA; 32111 MW; C791CB62FEA574E CRC64;

Query Match 27.2%; Score 270; DB 1; Length 289;
 Best Local Similarity 34.5%; Pred. No. 1,3e-16;
 Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

DR PROSITE: P500652; TNFR_NGFR.1; 1.
 DR PROSITE: P550050; TNFR_NGFR.2; 4.
 KW Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
 3D-structure.

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 277 CD40L RECEPTOR.
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 POTENTIAL.
 FT DOMAIN 216 277 CYTOSOLIC (POTENTIAL).
 FT DOMAIN 25 187 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 103 TNFR-CYS 2.
 FT REPEAT 104 144 TNFR-CYS 3.
 FT REPEAT 145 187 TNFR-CYS 4.
 FT DISULFID 26 37
 FT DISULFID 38 51
 FT DISULFID 41 59
 FT DISULFID 62 77
 FT DISULFID 83 103
 FT DISULFID 105 119
 FT DISULFID 111 116
 FT DISULFID 125 143
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

RESULT 4
 CD40_HUMAN STANDARD; PRT; 277 AA.
 AC P25942;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40) (TUMOR NECROSIS FACTOR RECEPTOR 5).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89356608; PubMed=2475341;
 RA Stamenkovic I., Clark E.A., Seed B.;
 RT "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas.";
 RL EMO J. 8:1403-1410(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 24-144.
 RX MEDLINE=97189482; PubMed=9037712;
 RA Bajorek J., Aruffo A.;
 RT "Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
 RL Proteins 27:59-70(1997).
 RN [3]
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., van Vlijmen H., Karsusas M., Hsu Y.-M.,
 RT "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 RN [4]
 RP FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 RN [5]
 RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 RN [6]
 RP TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
 RN [7]
 RP SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 RN [8]
 RP DATABASE: NAME-PROV: NOTE-CD guide CD40 entry;
 RN [9]
 RP WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".

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CC EMBL: X60592; CAA43045.1;
 CC PIR: S04460; S04460.
 CC PDB: 1CDF; 01-APR-97.
 CC MIM: 109535;
 CC INTERPRO: IPR001368;
 CC PFM: PFM00020; TNFR_C6; 4.

Query Match 26.3%; Score 261; DB 1; Length 277;
 Best Local Similarity 33.9%; Pred. No. 7,2e-16;
 Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

DR PROSITE: P500652; TNFR_NGFR.1; 1.
 DR PROSITE: P550050; TNFR_NGFR.2; 4.
 KW Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
 3D-structure.

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 277 CD40L RECEPTOR.
 FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 194 215 POTENTIAL.
 FT DOMAIN 216 277 CYTOSOLIC (POTENTIAL).
 FT DOMAIN 25 187 4 X TNFR-CYS.
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 103 TNFR-CYS 2.
 FT REPEAT 104 144 TNFR-CYS 3.
 FT REPEAT 145 187 TNFR-CYS 4.
 FT DISULFID 26 37
 FT DISULFID 38 51
 FT DISULFID 41 59
 FT DISULFID 62 77
 FT DISULFID 83 103
 FT DISULFID 105 119
 FT DISULFID 111 116
 FT DISULFID 125 143
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 277 AA; 30619 MW; BC8776EC2CA45680 CRC64;

RESULT 5
 CD40_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DT LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
 GN LYBR OR TNFR OR TNFRSF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=LIVER;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a hCDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 RN [2]
 RP FUNCTION:
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., van Arsden T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor.";
 RL Science 264:707-710(1994).
 CC -i- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN

IMMUNE DEVELOPMENT.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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EMBL: L04270; AAC36757.1; .

DR HSSP: P25942; 1CDF.

DR MIM: 600979; .

INTERPRO: IPR001368; .

PFAM: PF00020; TNFR_C6; 4.

DR PROSITE: PS00652; TNFR_NGFR_1; 2.

DR PROSITE: PS00500; TNFR_NGFR_2; 3.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 30

FT CHAIN 31 435

FT DOMAIN 31 227

FT TRANSMEM 228 248

FT DOMAIN 249 435

FT DOMAIN 42 211

FT REPEAT 42 81

FT REPEAT 82 124

FT REPEAT 125 168

FT REPEAT 169 211

FT DISULFID 43 58

FT DISULFID 59 72

FT DISULFID 62 80

FT DISULFID 83 98

FT DISULFID 101 116

FT DISULFID 104 124

FT DISULFID 126 132

FT DISULFID 139 148

FT DISULFID 142 167

FT DISULFID 170 185

FT CARBOHYD 40 40

FT CARBOHYD 177 177

FT SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 24.4%; Score 242.5; DB 1; Length 435;

Best Local Similarity 29.6%; Pred. No. 4.3e-14;

Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5;

QY 9 HYDPTGHLQDCAFGTYLKHQCTVRRKTLCPDPSHYSDSHMTDDECYVSCKE 68

DB 50 YLEPQ--HRTCSRCPPPTVYSAKCSRIIDVYCATCANSTVENHNNVLTICOLCRP-CDP 106

QY 69 LOSVQK--ECNRTNHRVCECEGRY-----LEIEFLKHRSCPSPG--GVVAGTPEERTV 120

DB 107 VMGLEELAPICSKRTQRCQPGMFCAMALECTHCELLSDCPTEALDELDEVCKGNH 166

QY 121 CKKCDGFGSGETSSKAPCIKHTNCTGGLLIQGNATHDNCVGNRE 169

DB 167 CVPKAGHFQNTSPSARCOPHTRCENOGIVEAAGTASDTCKNPLE 215

RESULT 6

CD40_BOVIN STANDARD; PRT; 269 AA.

ID ID

AC Q28203;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).

GN TNFRSF5 OR CD40.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

CC [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-97281252; PubMed-9135560;

RA Hirano A., Brown W.C., Estes D.M.;

RT "Cloning, expression and biological function of the bovine CD40

RT homologue: role in B-lymphocyte growth and differentiation in

RT cattle";

RL Immunology 90:294-300(1997).

CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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EMBL: U57745; AAC48710.1; .

DR HSSP: P25942; 1CDF.

DR INTERPRO: IPR001368; .

DR PFAM: PF00020; TNFR_C6; 4.

DR PROSITE: PS00652; TNFR_NGFR_1; 1.

DR PROSITE: PS00500; TNFR_NGFR_2; 1.

KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.

FT SIGNAL 1 19

FT CHAIN 20 269

FT DOMAIN 20 193

FT TRANSMEM 194 215

FT DOMAIN 216 269

FT DOMAIN 25 187

FT REPEAT 25 60

FT REPEAT 61 103

FT REPEAT 104 144

FT REPEAT 145 187

FT CARBOHYD 153 153

FT CARBOHYD 180 180

FT NON_TER 269

FT SEQUENCE 269 AA; 29983 MW; 746903F30F95F387 CRC64;

Query Match 22.9%; Score 227; DB 1; Length 269;

Best Local Similarity 33.1%; Pred. No. 6e-13;

Matches 57; Conservative 20; Mismatches 77; Indels 18; Gaps 5;

QY 8 LHYDEPG-----HQLDCKAPGTYLKHQCTVRRKTLCPDPSHYSDSHMTDDEC 59

DB 18 VHSPEATATCGEKQYRVNSLDCDLPPOGKLVNDCETEVSCQSGKGEFLSTNNREKVC 77

QY 60 --VYCSF--VEKELOSQVKECNRTNHRVCECEGRY-----LEIEFLKHRSCPSPG 112

DB 78 HEHRKCNPLGLRIQS---ESTLWDTICVCEBQDCHTSHTCECTPHSLCLPFGVKOT 134

QY 113 GTPRENTCKKCPDGFSGETSSKAPCIKHTNCTGGLLIQGNATHDNCV 164

DB 135 ATGLDITVCERCPLGFGFSNVSAFEKCHRWTSCKRKGLVEGHVGTNNTDVC 186

RESULT 7

VT2_SFVKA STANDARD; PRT; 325 AA.

ID ID

AC P25943;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).

GN TNFRSF5 OR CD40.

OS Shope fibroma virus (strain Kasza) (SFV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Leporipoxvirus.
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=87321103; PubMed=2820128;
 RA Upton C., Delange A.M., McFadden G.;
 RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
 RL telomeric region of the Shope fibroma virus genome";
 RN Virology 160:20-30(1987).
 [2]
 RP FUNCTION.
 RX MEDLINE=91307415; PubMed=1850261;
 RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrar T., Upton C.,
 RA McFadden G., Goodwin R.G.;
 RT "2 open reading frame from the Shope fibroma virus encodes a soluble
 form of the TNF receptor";
 RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
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 CC
 CC EMBL: M17433; NOT ANNOTATED_CDS.
 DR EMBL: A23727; CA01687.1; -;
 DR PIR: B43692; B43692.
 DR HSSP: P19438; 1TNR.
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 1.
 DR PROSITE: PS00652; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 325
 FT DOMAIN 27 186
 FT REPEAT 27 62
 FT REPEAT 63 104
 FT REPEAT 105 147
 FT REPEAT 148 186
 FT CARBOHYD 105 105
 FT CARBOHYD 181 181
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 SQ SEQUENCE 325 AA; 35132 MW; 81053039198A71E CRC64;

Query Match 22.8%; Score 226; DB 1; Length 325;
 Best Local Similarity 30.3%; Pred. No. 8, 7e-13;
 Matches 53; Conservative 18; Mismatches 68; Indels 36; Gaps 5;
 Oy 15 GHO-----LLDCKCAPGTLYLKOHCTVRRKTLVCPDPHSYDSTWHTSDECVYCSPVCKEL 69
 Db 30 GHDEKDGILCASCHPFGYASRLCGPSNTVYCSPECDGTFTASTNHPACVSCGPGCTGH 89
 Oy 70 QSKVQKQENRTHNRYCEEEERYLEIE-----FLKLRSCPPSGGVQAGTPERNYCKK 123
 Db 90 LSSQPDRTDRHRYCNCSTNYCLLKQNGCRICAPQTKCPAGYG-VSGHTRGDTLCEK 148
 Oy 124 CPDGFSGTSSKAPC-----IKHTNCSFEGLLILQKGNATHNV 163
 Db 149 CPHHTYSLSLSPERGCTSPNTYISVGFNLYPVNDTSCIT-----TAGHNEV 194

RESULT 8
 ID WT2_MXVL
 AC P29825;
 STANDARD;
 PRT; 326 AA.

DT 01-APR-1993 (rel. 25, Created)
 DT 01-APR-1993 (rel. 25, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91335768; PubMed=1651597;
 RA Upton C., Magen J.L., Schreiber M., McFadden G.;
 RT "Myxoma virus expresses a secreted protein with homology to the tumor
 RT necrosis factor receptor gene family that contributes to viral
 RT virulence";
 RL Virology 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC
 CC EMBL: M95181; AAA46632.1; -;
 DR EMBL: A23729; CA01688.1; -;
 DR PIR: A40566; GQVZML.
 DR HSSP: P19438; 1TNR.
 DR INTERPRO: IPR001368; -;
 DR PFAM: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186
 FT REPEAT 27 62
 FT REPEAT 63 104
 FT REPEAT 105 147
 FT REPEAT 148 186
 FT CARBOHYD 105 105
 FT CARBOHYD 181 181
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FE CRC64;

Query Match 21.2%; Score 211; DB 1; Length 326;
 Best Local Similarity 29.8%; Pred. No. 1, 7e-11;
 Matches 45; Conservative 20; Mismatches 64; Indels 22; Gaps 3;
 Oy 18 LLCDKCAPGTLYLKOHCTVRRKTLVCPDPHSYDSTWHTSDECVYCSPVCKELQSKQEN 77
 Db 38 LCTSCPPSGYARILGPGSDTYVCSPOKNETFTASTNHPACVSCGRCRGTGHLSEQSCD 97
 Oy 78 RTHNRYCEEEERYLEIE-----FLKLRSCPPSGGVQAGTPERNYCKKCPDGFSG 131
 Db 98 KTRDRCVDCSAGNYCLLKQNGCRICAPTKCPAGYG-VSGHTRGDTLCTKCPRYTSD 156
 Oy 132 ETSSKAPC-----IKHTNCS 147
 Db 157 AVSSTETCTSSSFNYSIVGFNLYPVNDTSCIT 187

RESULT 9
 ID VC22_VARY
 AC P34015;
 STANDARD;
 PRT; 349 AA.

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DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA Sheelkumov S.N., Blinov V.M., Sendakhev L.S.;
RT *Genes of variola and vaccinia viruses necessary to overcome the host
   protective mechanisms.;
   FEBS Lett. 319:80-83(1993).
   -1- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC -----
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CC -----
DR EMBL; X69198; CAA49137.1; -
DR EMBL; X67117; CAA47540.1; -
DR PIR; D36858; D36858.
DR PIR; S35987; S35987.
DR PIR; S46888; S46888.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_c6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Repeat.
KW DOMAIN 31 108 2 x TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
SQ SEQUENCE 349 AA; 38189 MW; DA5DA0B5C6E780EF CRC64;

Query Match. 21.2%; Score 210.5; DB 1; Length 349;
Best Local Similarity 30.0%; Pred. No. 2e-11;
Matches 48; Conservative 19; Mismatches 76; Indels 17; Gaps 4;

QY 10 YDPENG-----HQLCDKCAAGTYLKQHCYTRRKTLCYPCPDHSYTDSDWHTSDECV 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 25 YTPPGKCKDTEYKRHNHLCCLSCPGETYASRLCDSKTNTQCPSCSGFTSRNNHLPACL 84
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 YCSPVCKELQSVKQCNFTTHNRVCECGRYLEI-----EFCLEKHSQPSGVVQAGT 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 SCNGRCNSNQVETRSCNNTTHNRICCSFQYICLLGSSGCKACVQSYOTKGIQYG-VSGHT 143
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 115 PERNTVCKKCPDGEFSGETSSKAPCIKHTNCSFTGLLIQ 154
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 SVGDVICSPCGFGTYSHTVSSADKCEPVPN-NTFNVIDVE 182
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
ID TNRC_MOUSE STANDARD: PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LYBR OR TNFCR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GN [1]

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RP SEQUENCE FROM N.A.
RC STAIN-CVB: TISSUE=LUNG:
RX MEDLINE=96072804; PubMed=7594541.
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression".
RL J. Immunol. 155:5280-5280(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.".
RL Genomics 30:312-319(1995).
CC -I- PUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL; U29173; AAA69864.1; -
DR EMBL; L38423; AAB00846.1; -
DR EMBL; U30798; AAA81334.1; -
DR HSSP; P25942; 1CDF.
DR MGD; MG1:104875; LTBR.
DR INTERPRO: IPR001368; -
DR PFAM: PFO0020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGR_1; 2.
DR PROSITE; PS00500; TNFR_NGR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 1 415
FT DOMAIN 31 223 LYMPHOTOXIN-BETA RECEPTOR.
FT TRANSMEM 224 244 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 213 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 170 TNFR-CYS 3.
FT REPEAT 171 213 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL);
SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

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Db 107 VLGFEEVAPDTPSRKACRCOPGMSVCYLLDNECVHCEERLVLCOPSTEAVIDEIMDTD 166
 QY 119 TVCKKCDGFESESSKAPCIKHTNCSFTGILLIOGNATHDVGSGNNE 169
 Db 167 VNCVPCKRPHQNTSSPRACQPHTRCEIOGLVEADPGTSDTCKNPPE 217

RESULT 11
 NGFR_HUMAN
 ID NGFR_HUMAN STANDARD; PRT; 427 AA.
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051725; PubMed=3022937;
 RA Johnson D., Lananan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 Bothwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor.";
 RL Cell 47:545-554(1986).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=89096903; PubMed=2850481;
 RA Sehgal A., Patel N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 receptor gene.";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 CC EMBL: M14764; AAB59544.1; -;
 CC EMBL: M21621; AAA36363.1; -;
 CC PIR: A25218; GQHUN.
 CC HSSP: P07174; INGR.
 CC MIM: 162010; -;
 CC DR INTERPRO: IPR000488; -;
 CC DR INTERPRO: IPR001368; -;
 CC DR PFAM: PF00020; TNFR_c6; 4.
 CC DR PFAM: PF00051; death; 1.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 CC DR PROSITE: PS00650; TNFR_NGFR_2; 4.
 CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC KM Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 CC Phosphorylation; Signal.
 CC FT SIGNAL 1 28
 CC FT CHAIN 29 427
 CC FT DOMAIN 29 250 LOW-AFFINITY NERVE GROWTH FACTOR
 CC FT TRANSMEM 251 272 RECEPTOR.
 CC FT DOMAIN 273 427 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 31 189 POTENTIAL.
 CC FT CITOPLASMIC (POTENTIAL).
 CC FT DOMAIN 4 X TNFR-CYS.

FT REPEAT 31 65 TNFR-CYS 1.
 FT REPEAT 66 107 TNFR-CYS 2.
 FT REPEAT 108 147 TNFR-CYS 3.
 FT REPEAT 148 189 TNFR-CYS 4.
 FT DOMAIN 344 421 DEATH DOMAIN.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 64 BY SIMILARITY.
 FT DISULFID 67 83 BY SIMILARITY.
 FT DISULFID 86 99 BY SIMILARITY.
 FT DISULFID 89 107 BY SIMILARITY.
 FT DISULFID 109 122 BY SIMILARITY.
 FT DISULFID 125 138 BY SIMILARITY.
 FT DISULFID 128 146 BY SIMILARITY.
 FT DISULFID 149 164 BY SIMILARITY.
 FT DISULFID 167 180 BY SIMILARITY.
 FT DISULFID 170 188 BY SIMILARITY.
 FT DOMAIN 197 248 SER/THR-RICH.
 FT CARBOHYD 60 60 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 19.48; Score 192.5; DB 1; Length 427;
 Best Local Similarity 34.18; Pred. No. 8, 6e-10;
 Matches 45; Conservative 21; Mismatches 55; Indels 11; Gaps 5;

QY 20 CDKCAPGTLYKQHCQTVARKTLVCPDPH-SYTDHMTSDCEVCSPVCKELQSVKQECN 18
 Db 44 CKACNLGEGVAPGCGA-NQTVCEPCLDSTVFSVATEPCKRCTE-CVGLQSMAPG 101
 QY 79 THNRVCECEGRYLE-----IEFCLKHSRCPGSGVQAGTPRNATVCKKCPDGFSGET 133
 Db 102 ADNAVRCAGAYGYQDETTRGCAC---RVCAGSGLVFSCQDKNTVCCECPDGTYS 158
 QY 134 SSKAPCIKHTNC 145
 Db 159 NHVDPCLPCTVC 170

RESULT 12
 NGFR_RAT
 ID NGFR_RAT STANDARD; PRT; 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87115859; PubMed=3027580;
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 receptor.";
 RL Nature 325:593-597(1987).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93077038; PubMed=1446821;
 RA Metis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testostero-
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 RN [3]
 RP STRUCTURE BY NMR OF 334-418.
 RX MEDLINE=97449145; PubMed=9305641;
 RA Liepinsh E., Ilag L.L., Orling G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005(1997).

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-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NGF-4.
CC
-1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
CC -----
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CC -----
DR EMBL: X05137; CAA28783.1; -.
DR EMBL: X61269; -. NOT_ANNOTATED_CDS.
DR PIR: A26431; A26431.
DR PDB: INGR: 29-JUL-97.
DR INTERPRO: IPR000488; -.
DR INTERPRO: IPR001368; -.
DR PFAM: PF000020; TNFR_C6; 4.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW phosphorylation; signal; 3d-structure.
FT SIGNAL 1 29
FT CHAIN 30 425
FT
FT DOMAIN 30 251 LOW-AFFINITY NERVE GROWTH FACTOR
FT TRANSMEM 252 273 RECEPTOR.
FT DOMAIN 274 425 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 32 190 POTENTIAL.
FT REPEAT 32 66 CYTOPLASMIC (POTENTIAL).
FT REPEAT 67 108 4 X TNFR-CYS.
FT REPEAT 109 148 TNFR-CYS 1.
FT REPEAT 149 190 TNFR-CYS 2.
FT DOMAIN 198 249 TNFR-CYS 3.
FT DOMAIN 354 419 TNFR-CYS 4.
FT SER/THR-RICH.
FT DEATH DOMAIN.
FT DISULFID 33 44 BY SIMILARITY.
FT DISULFID 45 58 BY SIMILARITY.
FT DISULFID 48 65 BY SIMILARITY.
FT DISULFID 68 84 BY SIMILARITY.
FT DISULFID 87 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT DISULFID 110 123 BY SIMILARITY.
FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 129 147 BY SIMILARITY.
FT DISULFID 150 165 BY SIMILARITY.
FT DISULFID 168 181 BY SIMILARITY.
FT DISULFID 171 189 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 425 AA; 45432 MW; B2E15D94D3827F8 CRC64;
SQ
Query Match 19.0%; Score 188.5; DB 1; Length 425;
Best Local Similarity 33.3%; Pred. NO. 1.9e-09;
Matches 43; Conservative 23; Mismatches 58; Indels 5; Gaps 4;
OY 20 CDKCAPGYLYLKHCHVRRKTLCPDPD- SYTDSMHTSDECVYSPYCKLQSYKQECNR 78
DB 45 CKACMGSGVADPCGA-NQTYCEPCLDVTSDVVSATPECKPCTE-CLGLQSKSPACE 102
OY 79 TNHRYCECEGRHYLEI--FCLKHRSCKPPGSGVQAGTPEKTYCKKCPDGFSGSETSK 136
DB 103 ADDAVCAICAYGYODEEFGHCACGVCVSGSLVFSQDCKQNTVCEBCEPGLTSDANHV 162
OY . 137 APCIKHTNC 145

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ID	NGFR_CHICK	STANDARD;	PRT;	416 AA.
RESULT	13			
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AC	P18519			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)			
GN	(GP80-1ANGFR) (p75 ICD).			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
NC	Gallus.			
NC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RA	MEDLINE=90166579; PubMed=2560385;			
RA	Large T.H., Westkamp G., Helder J.C., Radeke M.J., Misko T.P.,			
RA	Shooter E.M., Reichardt L.F.;			
RT	"Structure and developmental expression of the nerve growth factor			
RT	receptor in the chicken central nervous system."			
RL	Neuron 2:1123-1134(1989).			
RL	[2]			
RP	SEQUENCE OF 21-416 FROM N.A.			
RX	MEDLINE=90152140; PubMed=2154393;			
RA	Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;			
RT	"Structure and developmental expression of the chicken NGF receptor."			
RL	Dev. Biol. 137:287-304(1990)			
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF			
CC	NT-3, AND NT-4.			
CC	-1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE			
CC	BOND FORMATION.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- PIM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
DR	PIR: J00006; J00006.			
DR	PIR: A60504; A60504.			
DR	HSP: P07174; INGR.			
DR	INTERPRO: IPR000488; -			
DR	INTERPRO: IPR001368; -			
DR	PRAM; PF00020; TNFR_C6; 4.			
DR	PFAM; PF00531; death; 1.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE; PS00505; TNFR_NGFR_2; 3.			
DR	PROSITE; PS00017; DEATH DOMAIN; 1.			
KW	Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;			
KW	phosphorylation; Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	416	LOW-AFFINITY NERVE GROWTH FACTOR
FT				RECEPTOR.
FT	DOMAIN	29	239	POTENTIAL.
FT	TRANSMEM	240	261	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	262	416	POTENTIAL.
FT	DOMAIN	23	181	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	23	57	4 X TNFR-CYS.
FT	REPEAT	58	100	TNFR-CYS 1.
FT	REPEAT	101	140	TNFR-CYS 2.
FT	REPEAT	141	181	TNFR-CYS 3.
FT	DOMAIN	188	236	TNFR-CYS 4.
FT	DOMAIN	333	410	SEK/THR-RICH.
FT	DISULFID	24	35	DEATH DOMAIN.
FT	DISULFID	36	49	BY SIMILARITY.
FT	DISULFID	39	56	BY SIMILARITY.
FT	DISULFID	59	75	BY SIMILARITY.
FT	DISULFID	78	91	BY SIMILARITY.
FT	DISULFID	81	99	BY SIMILARITY.
FT	DISULFID	101	114	BY SIMILARITY.

Search completed: January 27, 2001, 11:24:57
Job time: 139 sec

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RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD:
RX MEDLINE=94085794; PubMed=8262389;
RA Schwarz H., Tuckwell J., Lotz M.;
RT "A receptor induced by lymphocyte activation (ILA): a new member of
RL the human nerve-growth-factor/tumor-necrosis-factor receptor
RN family."
RN Gene 134:295-298(1993).
RP [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD:
RX MEDLINE=95347766; PubMed=7622190;
RA Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA Kwon B.S.;
"Characterization of human homologue of 4-1BB and its ligand.";
Immunol. Lett. 45:67-73(1995).
CC -I- FUNCTION: RECEPTOR FOR THE POTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T
CC CELLS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
CC -----
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DR EMBL: U03397; AAA53133.1;
DR EMBL: L12964; AAA62478.1;
DR HSSP: P19438; 1EXT.
DR MIM: 602250;
DR INTERPRO: IPR001368;
DR PFAM: PF00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KM Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 255 4-1BB LIGAND RECEPTOR.
FT DOMAIN 18 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 213 POTENTIAL.
FT DOMAIN 214 255 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 159 3 X TNFR-CYS.
FT REPEAT 47 86 TNFR-CYS 1.
FT REPEAT 87 118 TNFR-CYS 2.
FT REPEAT 119 159 TNFR-CYS 3.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 107 107 K->R (IN REF. 2).
SQ SEQUENCE 255 AA; 27899 MM; F3A563FE5EF00460 CRC64;

Query Match 16.8%; Score 167; DB 1; Length 255;
Best Local Similarity 27.5%; Pred. No. 8.3e-08;
Matches 44; Conservative 24; Mismatches 72; Indels 20; Gaps 6;

OY 8 LHAYDETHQLLDCRCAPGYLKQHCIVTRKTLICVPCPDHSTYDS--WHTSDECVYCSPIV 65
DB 16 LNFERTSLQDPDCSNCPAGTF----CDNNRNQICSPCPNPSSTSSAGGORTCDICRCKGV 71
OY 66 KELOSVAQECNRHNRVCECEEGRYLEIFRC-LKHSRCPPGSGVVGAGTPERNVTCKKC 124
DB 72 FR---TRKESSTSNACDCTPGFPHCLGAGCSMCEQDCQKQOELTKKG-----CRDC 120
OY 125 PDGFSGETSNAPCIKHTNCGSTFGLLLIQKGNATHDNVC 164
DB 121 CFGTFNDQ--KRGICRPWNTCSLDGKSVLVNGTKERDYYC 158
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:23:12 ; Search time 25.38 Seconds

(without alignments)
462.837 Million cell updates/sec

Title: US-09-389-545-2_COPY_22_194

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Working table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	30.2	459	2	148854
2	298	30.0	461	1	A35356
3	297	29.9	474	1	B38634
4	270	27.2	289	2	A46515
5	270	27.2	305	2	A46476
6	261	26.3	277	2	A60771
7	242.5	24.4	435	2	154182
8	226	22.8	325	2	B43692
9	211	21.2	326	1	GOVZML
10	210.5	21.2	348	1	T28623
11	210.5	21.2	349	2	D36858
12	209.5	21.1	349	2	D72175
13	192.5	19.4	427	1	GOHUN
14	188.5	19.0	425	1	A26431
15	184	18.5	416	1	UN0006
16	177	17.8	256	2	B32393
17	167	16.8	255	2	138426
18	166	16.7	255	2	JT0752
19	163	16.4	271	2	S12783
20	160	16.1	455	1	GOHUT1
21	159	16.0	454	1	GOHST1
22	159	16.0	454	2	157826
23	159	16.0	461	2	JC4302
24	152	15.3	272	2	148700
25	148	14.9	461	1	GOHRT1
26	145	14.6	277	2	137552
27	144.5	14.6	314	2	137383
28	144	14.5	335	2	A40036
29	139	14.0	595	2	A42086

30	137.5	13.8	324	2	JC2395	Fas anti...
31	137	13.8	327	2	A46484	apoptosis
32	125	12.6	899	2	GO2428	subtilisin-like pr
33	125	12.6	915	2	JC6148	subtilisin-like pr
34	125	12.6	1680	2	A43434	furin (EC 3.4.21.7
35	120	12.1	786	2	A48456	ococyst wall protei
36	120	12.1	1252	2	S36016	ococyst wall protei
37	119.5	12.0	1548	2	S34583	serine protease
38	118.5	11.9	260	1	A46517	CD27 antigen precu
39	118.5	11.9	1609	1	MMHUB2	laminin gamma-1 ch
40	115.5	11.6	1111	2	T26972	hypothetical prote
41	114.5	11.5	643	2	T25473	hypothetical prote
42	113.5	11.4	1607	1	MMMSB2	laminin gamma-1 ch
43	111	11.2	1955	1	ACGH	aglin precursor -
44	109.5	11.0	250	1	A49053	CD27 antigen precu
45	109.5	11.0	667	2	A48579	trophozoite surfac

ALIGNMENTS

RESULT 1
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gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C.Accession: 148854
R.Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A.Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A.Reference number: 148854; MUID:95178848
A.Accession: 148854
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-459 <RES>
A.Cross-references: EMBL:X76401; NID:q433830; PIDN:CA53981.1; PID:q.4831
A.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F.151-188/Domain: NGF receptor repeat homology <NGF>

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Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;
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DB 17 YKPEGEYEQISOEYDRKAKOMCAKCPGQYVKKHFCNKTSDTVCADEASWYQVMNQF 76
QY 57 DDCVYCSPYCKELOSVKQECNFTNHRVCECEGRYLETF-----CLKHRCSPGSGY 109
DB 77 KRLCSGSSCSTDOYETRACTKOQNRVCCAGRCALRKHGSGRCQKRLSKCGPGF 136
QY 110 VQAGPERNTVCKKCPDGFSGETSSKAPCIRKHTNCSFFGLLLQKGNATHDNCVS 155
DB 137 ASSRAPNGWNLCKACAPGFSTSTSDVCBPHRIS---ILAIIPGNASTDVAICA 194
RESULT 2
A35356
tumor necrosis factor receptor type 2 precursor - human
N.Alternate names: 75K tumor necrosis factor receptor
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A35356; A36475; A48416; A36007; A23666; B35010; 138094
R.Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
Science 248, 1019-1023, 1990
A.Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A.Reference number: A35356; MUID:90260639
A.Accession: A35356
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-461 <SMI>
A.Cross-references: GB:M32315; NID:g189185; PIDN:AA53929.1; PID:g189186

R:Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.R.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring A:Reference number: A36475; MUID:91045991
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758
 R:Dombo, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:q235648; PIDN:AA19824.1; PID:q235649
 A:Note: Sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration A:Reference number: A36007; MUID:90349572
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
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 A:Cross-references: GB:M55857; NID:q339751; PIDN:AA63262.1; PID:q339752
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20331-20338, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis A:Reference number: A23666; MUID:91056048
 A:Accession: A23666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A:Reference number: A35010; MUID:90110215
 A:Accession: B35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kühnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934
 A:Accession: I38094
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 A:Molecule type: DNA
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 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: the list of introns is incomplete
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 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
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 F:23-416/Product: tumor necrosis factor receptor type 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG3>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.0%; Score 298; DB 1; Length 461;

Best Local Similarity 35.6%; Pred. No. 1.7e-16;
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 32 YAPPGSTCRRLREYDDTADMCCKSPGQAHAFVCTKTDYDSCDSEDTYQJLMMV 91
 58 ECVYCSFVCKELQSVKQECNRTHNRCCEGRYLEI-----EFLKHSRCPGSGV 111
 92 ECLSCGSRGSSDQVETACRQNRICRPRGWCALSKQEGRLCAPLKRKRGRGFGVAR 151
 112 AGPERNTVCKKCPDGFSSGTSKAPCIRKTNSTGGLILQKGNATHNVC 165
 152 PGETSDVCKPCAPGFSMTSTSDICRPHQICNVVAI-----PGNSMAPVCT 201
 RESULT 3
 B38634
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-J 1999
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tarrapija, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wc, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto A:Reference number: A38634; MUID:91187885
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEM>
 A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199827
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Brannan, C.I.; Copeland, N.G.; Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors A:Reference number: A40254; MUID:91246168
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:q199827; PIDN:AAA39752.1; PID:q199827
 R:Kisonegishis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine TNF receptor A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X87128; NID:q809043; PIDN:CAA60618.1; PID:q809044
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-110/Domain: NGF receptor repeat homology <NG4>
 F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 29.9%; Score 297; DB 2; Length 474;
 Best Local Similarity 35.2%; Pred. No. 2e-16;
 Matches 62; Conservative 17; Mismatches 73; Indels 24; Gaps 3;
 10 YDPETG-----OLCDKCAPGTLYKOHCVRRKTLCPDPDHYTDSMTSP 57
 32 YKPEPGEGCISQIDRYDKAMCCACRPPQYVHFCNKTSDFVACADCEASMTYVNNQF 91
 57 DECVYCSFVCKELQSVKQECNRTHNRCCEGRYLEI-----CLKHRSRCPGSGV 109
 92 RTCLSCSSSTTQVETRACTKQNRVCAEAGYCAKLKTHSGSCRCRMLSYCGPFGV 151
 110 VQAGTPEPRNTVCKKCPDGFSSGTSKAPCIRKTNSTGGLILQKGNATHNVC 166
 152 ASSRAPNGNVLCRACAGTFTSDTTSIDVCRPHRIS-----ILAIQGNASTDAVCA 203

R;Blinov, V.M.

100

F:67-108/Domain: NGF receptor repeat homology <NG2>
 F:109-147/Domain: NGF receptor repeat homology <NG3>
 F:149-189/Domain: NGF receptor repeat homology <NG4>
 F:191-248/Region: serine/threonine-rich
 F:251-272/Domain: transmembrane #status predicted <TRM>
 F:273-427/Domain: intracellular #status predicted <INT>
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 192.5; DB 1; Length 427;
 Best Local Similarity 34.1%; Pred. No. 3.2e-08;
 Matches 45; Conservative 21; Mismatches 55; Indels 11; Gaps 5;

OY 20 CDKAPGTYLKHCHTTRKRLTLCVPCPDH-SYTDMSHTSDECVYSPYCKELQSVKQECNR 78
 DB 44 CKACNLGEGVQPCGA-NQTVCEPCLDSVTSDVSATPECKPCTE-CVGLHSMAPCPE 101
 OY 79 THNRVCEEBEGRYLE-IEFLKHSRCPGSGVQAGTPERNYVCKKCPDPFGSGETS 133
 DB 102 ADDAVRCRAYGYODETGHCEAC--RVCEAGSGLVFCODKONTVCEECPCDTYSDEA 158
 OY 134 SSKAPCIKHTNC 145
 DB 159 NHVDPCLPCTVC 170

RESULT 14
 A:26431
 nerve growth factor receptor precursor, low affinity - rat

N:Alternate names: NGF receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A26431; PMID:956756
 R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
 Nature 325, 593-597, 1987

A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
 A:Reference number: A26431; MUID:87115859
 A:Accession: A26431

A:Molecule type: mRNA
 A:Residues: 1-425 <RAD>
 A:Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

R:Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
 Gene 121, 247-254, 1992
 A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid

A:Reference number: PH1229; MUID:93077038
 A:Accession: PH1229
 A:Molecule type: DNA

A:Residues: 1-20 <MEM>
 A:Cross-references: GB:X61269
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w
 C:Genetics:

Introns: 20/3

Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
 F:1-59/Domain: signal sequence #status predicted <SIG>
 F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
 F:30-251/Domain: extracellular #status predicted <EXT>
 F:33-66/Domain: NGF receptor repeat homology <NG1>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-148/Domain: NGF receptor repeat homology <NG3>
 F:150-190/Domain: NGF receptor repeat homology <NG4>
 F:198-249/Region: serine/threonine-rich
 F:252-273/Domain: transmembrane #status predicted <TRM>
 F:274-425/Domain: intracellular #status predicted <INT>
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.0%; Score 188.5; DB 1; Length 425;
 Best Local Similarity 33.3%; Pred. No. 6.7e-08;
 Matches 43; Conservative 23; Mismatches 58; Indels 5; Gaps 4;

OY 20 CDKAPGTYLKHCHTTRKRLTLCVPCPDH-SYTDMSHTSDECVYSPYCKELQSVKQECNR 78
 DB 45 CKACNLGEGVQPCGA-NQTVCEPCLDSVTSDVSATPECKPCTE-CVGLHSMAPCPE 102
 OY 79 THNRVCEEBEGRYLE-IEFLKHSRCPGSGVQAGTPERNYVCKKCPDPFGSGETS 136
 DB 103 ADDAVRCRAYGYODETGHCEACSVCEAGSGLVFCODKONTVCEECPCDTYSDEANHV 162

OY 137 APCIKHTNC 145
 DB 163 DPCLPCTVC 171

RESULT 15
 JN0006
 nerve growth factor receptor, low affinity precursor - chicken

N:Alternate names: NGF receptor
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JN0006; A60504
 R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R
 Neuron 2, 1123-1134, 1989
 A:Title: Structure and developmental expression of the nerve growth factor receptor 1

A:Reference number: JN0006; MUID:9016579
 A:Accession: JN0006
 A:Molecule type: mRNA
 A:Residues: 1-416 <LAR>
 A:Experimental source: embryonic chick brain
 R:Heuer, J.G.; Falemie-Nahie, S.; Wheeler, E.F.; Bothwell, M.
 Dev. Biol. 137, 287-304, 1990
 A:Title: Structure and developmental expression of the chicken NGF receptor.
 A:Reference number: A60504; MUID:90152140
 A:Accession: A60504

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <RNI>
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all
 C:Comment: This protein is thought to form a high-affinity receptor when it associate
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
 F:21-239/Domain: extracellular #status predicted <EXT>
 F:24-57/Domain: NGF receptor repeat homology <NG1>
 F:59-100/Domain: NGF receptor repeat homology <NG2>
 F:101-139/Domain: NGF receptor repeat homology <NG3>
 F:141-181/Domain: NGF receptor repeat homology <NG4>
 F:182-237/Region: serine/threonine-rich
 F:240-261/Domain: transmembrane #status predicted <TRM>
 F:262-416/Domain: intracellular #status predicted <INT>
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.5%; Score 184; DB 1; Length 416;
 Best Local Similarity 30.9%; Pred. No. 1.3e-07;
 Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

OY 20 CDKAPGTYLKHCHTTRKRLTLCVPCPDH-SYTDMSHTSDECVYSPYCKELQSVKQECNR 78
 DB 36 CKACNLGEGVQPCGV-NQTVCEPCLDSVTSDVSATPECKPCTQ-CVGLHSMAPCPE 93
 OY 79 THNRVCEEBEGRYLEIE-IEFLKHSRCPGSGVQAGTPERNYVCKKCPDPFGSGETS 135
 DB 94 SDAVRCRAYGYODELSSGCKSCICEVGFGLFPCROSDQIVCEECPCGTSDANF 152
 OY 136 KAPCIKHTNSTFGLLQKGNATHDNC 164
 DB 153 VDPCLPCTICEE-NEVMWKECTATSDAEC 180

Search completed: January 27, 2001, 11:23:14

Sat Jan 27 11:26:07 2001

Job time: 37 sec

us-09-389-545-2 copy_22_194.rpr

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:23:46 ; Search time 32.57 Seconds

(without alignments)
181.625 Million cell updates/sec

Title: US-09-389-545-2_COPY_22_194
Perfect score: 993
Sequence: 1 ETLPKYLHDPETGHLQC.....QKGNATHDNCVSGNREATQK 173

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_36:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
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- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
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- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	993	100.0	401	18	Mouse osteoprotegerin
2	936	94.3	401	18	Rat osteoprotegerin
3	887	89.3	197	17	Mutated OCIF, OCIF
4	887	89.3	272	17	Mutated OCIF, OCIF
5	887	89.3	321	17	Mutated OCIF, OCIF
6	887	89.3	326	17	Mutated OCIF, OCIF
7	887	89.3	327	17	Mutated OCIF, OCIF
8	887	89.3	349	20	Human FTHMA-070 pa
9	887	89.3	351	17	Mutated OCIF, OCIF
10	887	89.3	380	17	Mature osteoclasto
11	887	89.3	390	17	Human tumour necro
12	887	89.3	391	19	Human OCIF genome

13	887	89.3	393	17	R99948
14	887	89.3	395	19	M57636
15	887	89.3	399	17	R99942
16	887	89.3	401	17	R99932
17	887	89.3	401	17	R99934
18	887	89.3	401	17	R99925
19	887	89.3	401	17	R99931
20	887	89.3	401	18	M38345
21	887	89.3	401	19	M53239
22	887	89.3	401	19	Y05742
23	887	89.3	401	20	W95030
24	887	89.3	401	20	M83926
25	887	89.3	401	21	Y43400
26	884	89.0	401	17	R99933
27	883	88.9	401	19	M57635
28	877	88.3	401	17	R99935
29	861	86.7	187	17	R99950
30	861	86.7	187	17	R99950
31	688	69.3	360	17	R99936
32	654	65.9	360	17	R99938
33	650	65.5	359	17	R99939
34	642	64.7	143	17	R99946
35	617	62.1	359	17	R99937
36	596	60.0	154	17	R99929
37	594.5	59.9	145	17	R99930
38	443	44.6	106	17	R99947
39	420	42.3	245	20	Y28449
40	420	42.3	271	20	Y42184
41	420	42.3	300	19	M66102
42	420	42.3	300	19	M63622
43	420	42.3	300	20	Y03099
44	420	42.3	300	20	Y42182
45	420	42.3	300	20	Y17479

ALIGNMENTS

RESULT 1	
W38344	
ID	W38344 standard; Protein: 401 AA.
XX	
AC	W38344:
XX	
DT	20-APR-1998 (first entry)
XX	
DE	Mouse osteoprotegerin.
XX	
KW	Osteoprotegerin: antibody; diagnosis; affinity purification;
KW	recombinant production; transgenic animal; treatment; preventio
KW	antisense oligonucleotide; probe; detection; screening; mouse;
KW	bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW	hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW	osteolytic metastasis; periodontal bone loss; bone necrosis;
KW	osteopenia; murine.
XX	
OS	Mus sp.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS 90..1295
FT	/*tag= a
FT	/product= osteoprotegerin
XX	
PN	DE19654610-A1.
XX	
PD	26-JUN-1997.
XX	
PF	20-DEC-1996; 96DE-1054610.
XX	
PR	03-SEP-1996; 96US-0706945.
PR	22-DEC-1995; 95US-0577788.
XX	
PA	(AMGE-) AMGEN INC.

Mutated OCIF, OCIF
Modified OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Full length osteoc
Mutated OCIF, OCIF
Human osteoprotege
Human OCIF genome
Human OCIF genome
Tumour necrosis fa
Human FTHMA-070 pr
Osteoprotegerin pro
Mutated OCIF, OCIF
TPI receptor prote
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Osteoclastogenesis
Mutated OCIF, OCIF
A human tumour nec
Human mFTHMA-070 pr
Amino acid sequenc
Human tumour necro
Human FTHMA-070 pr
Memorial tumour n

XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS.
PI
XX WPI: 1997-334271/31.
DR N-PSDB: T96062.
XX

XX Nucleic acid encoding osteoprotegerin - useful for treatment of
PT diseases involving excessive bone loss, e.g. osteoporosis
XX
XX
PS Claim 23; Pages 106-107; 182pp; German.

XX The present sequence is mouse osteoprotegerin (OPG). Anti-OPG
CC antibodies can be used in OPG diagnostic assays, and as affinity
CC purification materials. The OPG cDNA can be used to express
CC recombinant OPG and to generate transgenic animals. It can also
CC be used to regulate the level of OPG in mammals, specifically to
CC increase OPG levels, however the use of antisense sequences is
CC also contemplated. Fragments of the cDNA can be used as probes to
CC detect OPG expressing cells and tissue, and to screen cDNA
CC libraries for related sequences. OPG can be used to treat or
CC prevent bone diseases, specifically excessive bone loss, e.g.
CC osteoporosis, Paget's disease, hypercalcaemia,
CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC osteolytic metastases, periodontal bone loss, bone necrosis and
CC osteopaenia.

Sequence 401 AA;

Query Match 100.0%; Score 993; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ETLPPKYLHYHPETGSHQLCDKCAPGYLKQHCYVRRKTLCPDHSYTDMSWTSDECV 60
DB 22 etlppkylyhyhpetsghqlcdkcapgylykqhcvrrtklcvppdhsytdmswtsdecv 81
OY 61 YCSPVCKELQSVKQECNTRHNRCVCEEGRYLEIFCLKHNSCPGSGVVOAGTPERNV 120
DB 82 ycspvckelqsvkqecntrhnrcvceegrylelefcikhrscppsgsvvqagtpervntv 141
OY 121 CKKPDGFFSGSETSKAPCIRKHTNCSFGLLIOGNATHDNCVSGNREARQK 173
DB 142 ckcpdggfsgsetskapcirkhtncstfgllilqkgnathdncvsgnreataqk 194

RESULT 2
W38343

ID W38343 standard; Protein; 401 AA.

AC W38343;

DT 20-APR-1998 (first entry)

Rat osteoprotegerin.

KW Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
KW recombinant production; transgenic animal; treatment; prevention;
KW antisense oligonucleotide; probe; detection; screening;
KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; bone necrosis;
KW osteopaenia.

OS Rattus sp.

PN DE19654610-A1.

PD 26-JUN-1997.

PF 20-DEC-1996; 96DE-1054610.

PR 03-SEP-1996; 96US-0706945.

PR 22-DEC-1995; 95US-0577788.
XX
XX (AMGE-) AMGEN INC.
XX

XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
PI
XX WPI: 1997-334271/31.
DR N-PSDB: T96061.

XX Nucleic acid encoding osteoprotegerin - useful for treatment of
PT diseases involving excessive bone loss, e.g. osteoporosis
XX
XX
PS Claim 23; Pages 102-104; 182pp; German.

XX The present sequence is rat osteoprotegerin (OPG). Anti-OPG
CC antibodies can be used in OPG diagnostic assays, and as affinity
CC purification materials. The OPG cDNA can be used to express
CC recombinant OPG and to generate transgenic animals. It can also
CC be used to regulate the level of OPG in mammals, specifically to
CC increase OPG levels, however the use of antisense sequences is
CC also contemplated. Fragments of the cDNA can be used as probes to
CC detect OPG expressing cells and tissue, and to screen cDNA
CC libraries for related sequences. OPG can be used to treat or
CC prevent bone diseases, specifically excessive bone loss, e.g.
CC osteoporosis, Paget's disease, hypercalcaemia,
CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC osteolytic metastases, periodontal bone loss, bone necrosis and
CC osteopaenia.

Sequence 401 AA;

Query Match 94.3%; Score 936; DB 18; Length 401;
Best Local Similarity 93.6%; Pred. No. 5.8e-74;
Matches 161; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 ETLPPKYLHYHPETGSHQLCDKCAPGYLKQHCYVRRKTLCPDHSYTDMSWTSDECV 60
DB 22 etlppkylyhyhpetsghqlcdkcapgylykqhcvrrtklcvppdhsytdmswtsdecv 81
OY 61 YCSPVCKELQSVKQECNTRHNRCVCEEGRYLEIFCLKHNSCPGSGVVOAGTPERNV 120
DB 82 ycspvckelqsvkqecntrhnrcvceegrylelefcikhrscppsgsvvqagtpervntv 141
OY 121 CKKPDGFFSGSETSKAPCIRKHTNCSFGLLIOGNATHDNCVSGNREARQK 172
DB 142 ckcpdggfsgsetskapcirkhtncstfgllilqkgnathdncvsgnreataqk 193

RESULT 3
R99945

ID R99945 standard; Protein; 197 AA.

AC R99945;

DT 23-APR-1997 (first entry)

DE Mutated OCIF, OCIF-CD1.

KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorpti
KW osteoporosis.
KW

OS Synthetic.

OS Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note="Signal peptide"
22..197

PN W09626217-A1.

PD 29-AUG-1996.

PD 29-AUG-1996.
XX
XX 20-FEB-1996; 96WO-JP00374.
PF
XX 21-JUL-1995; 95JP-0207508.
PR 20-FEB-1995; 95JP-0054977.
PR
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
PI GOTO M, Hiashio K, Kobayashi F, Mochizuki S, Morinaga T,
PI Nakagawa N, Shima N, Tsuda E, Ueda M, Iano K, Yasuda H;
XX WPI: 1996-402320/40.
DR N-PSDB: T33174.
XX
PT DNA encoding osteoclastogenesis inhibitory factor protein - use
PT for bone resorption control, esp. treatment of osteoporosis
XX
XX
PS Claim 68: Page 121-122; 183pp; Japanese.
XX
CC This sequence represents a mutated version of the full length
CC osteoclastogenesis inhibitory factor (OCIF) of the invention. Thi
CC sequence represents OCIF-CD2 in which amino acids 252-380 of t
CC mature OCIF protein are deleted. The OCIF of the invention
CC has a molecular weight by SDS-PAGE of 60 kD under reducing condit
CC and 120 kD under non-reducing conditions. The protein is adsorbed on
CC cation-exchangers or heparin and its activity is lowered after 10 mins at
CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70
CC deg.C. OCIF is useful in the control of bone resorption and the treat
CC in the treatment and prevention of disorders of bone resorption,
CC osteoporosis.

Query Match	89.3%	Score 887	DB 17	Length 272
Best Local Similarity	87.3%	Pred. No. 6.9e-70		
Matches 151	Conservative 7	Mismatches 15	Indels 0	gaps 0
Db	1	ETLPKRYLHYDERGHOILLODKCAPGYLKHQCTVRRKRTLCVPRCPDHSTDSMHNSDR'V	40	
	22	etfppkylhydeetsrqllcdkcpqgtylkqntcakwktvcapcpdhyytldswhnsde	81	
QY	61	YCSPIVCKELQSVKQECNNTNHNREVCCEGRYLEIEFCLLKHRSQPGSGVVOAGTPERNTV	120	
	82	yvspckelqyvkqecntnhrvceckegryleiefclkhrcspqgfygvvgagtpern	141	
QY	121	CKKCPDGFSGFTSSKAPCIKHTNCSFTGLLILOKGNATHDVCNCGNREATOR	173	
	142	ckrcpdgffsnetsskapcrkhtncsfvgllltqgualhndhicsgnsesqk	194	
Db				
RESULT	5			
R99949	R99949	standard: Protein; 321 AA.		
AC	AC	R99949;		
XX	XX			
DT	DT	23-APR-1997 (first entry)		
XX	XX			
DE	DE	Mutated OCIF, OCIF-CSph.		
XX	XX			
KM	KM	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone res		
XX	XX	osteoporosis.		
OS	OS	Synthetic.		
XX	XX			
Key	Key	Location/Qualifiers		
FT	FT	1..21		
FT	FT	/note= "Signal peptide"		
FT	FT	22..321		
FT	FT	/note= "Mature OCIF-CSph"		

XX MO9626217-A1.
 XX 29-AUG-1996.
 XX 20-FEB-1996; 96WO-JP00374.
 XX 21-JUL-1995; 95JP-0207508.
 XX 20-FEB-1995; 95JP-0054977.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T,
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
 XX WPI: 1996-402320/40.
 DR N-PSDB: T33179.
 XX DNA encoding osteoclastogenesis inhibitory factor protein - useful
 PT for bone resorption control, esp. treatment of osteoporosis
 XX Claim 83; Page 128-129; 183pp; Japanese.
 XX This sequence represents a mutated version of the full length
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 CC sequence represents OCIF-CspH in which amino acids 298-380 of the mature
 CC OCIF protein are replaced by Ser-Leu-Asp. These changes are caused by
 CC the introduction of a restriction site in the DNA encoding this protein.
 CC The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD
 CC under reducing conditions and 120 kD under non-reducing conditions. The
 CC protein is adsorbed onto cation-exchangers or heparin and its activity is
 CC lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost
 CC after 10 mins at 90 deg.C. OCIF is useful in the control of bone
 CC resorption and therefore in the treatment and prevention of disorders
 CC of bone resorption, e.g. osteoporosis.
 XX Sequence 321 AA;
 SQ

Query Match 89.3%; Score 887; DB 17; Length 321;
 Best Local Similarity 87.3%; Pred. No. 8.3e-70;
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETLPPKYLHYDPETGHOGLCDKCAPGTYLKHCHTVRRKTLCPDPSHYTSDSWHTSDDEV 60
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 22 etfppkylyhydeetshqllcdkcpptgylkqhctakwktvcapcpdhytswhtsdecl 81
 QY 61 YCSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFLKLRSCPPGSGVQAGTPERNTV 120
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 82 ycspvckelqsvkqecnrtnhrvcecegryleiefclkhscppgfgvvagqlperntv 141
 QY 121 CKKCPDGFSGSETSSKAPCIKHTNCGSTFGLLILQGNATHNNVCSGNREATOR 173
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 142 ckrcpdgffsnetsskapeckrhncsvfgllllctqgnathndnlesgnsesctq 194

RESULT 6
 R99940
 ID R99940 standard; Protein; 326 AA.
 XX R99940;
 XX AC
 XX 23-APR-1997 (first entry)
 XX Mutated OCIF, OCIF-DDD1.
 XX DE
 XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
 XX osteoporosis.
 XX OS
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT

FT /note="Signal peptide"
 FT Protein 22..326
 FT /note="Mature OCIF-DDD1"
 FT MISC-difference 198..199
 FT /note="Position of deletion, delta 178-252"
 XX MO9626217-A1.
 XX 29-AUG-1996.
 XX 20-FEB-1996; 96WO-JP00374.
 XX 21-JUL-1995; 95JP-0207508.
 XX 20-FEB-1995; 95JP-0054977.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T,
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
 XX WPI: 1996-402320/40.
 DR N-PSDB: T33170.
 XX DNA encoding osteoclastogenesis inhibitory factor protein - useful
 PT for bone resorption control, esp. treatment of osteoporosis
 XX Claim 56; Page 113-114; 183pp; Japanese.
 XX This sequence represents a mutated version of the full length
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 CC sequence represents OCIF-DDD1 in which amino acids 178-252 of the
 CC mature OCIF protein are deleted. The OCIF of the invention
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
 CC cation-exchangers or heparin and its activity is lowered after 10 mins
 CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
 CC deg.C. OCIF is useful in the control of bone resorption and therefore
 CC in the treatment and prevention of disorders of bone resorption, e.g.
 CC osteoporosis.
 XX Sequence 326 AA;
 SQ

Query Match 89.3%; Score 887; DB 17; Length 326;
 Best Local Similarity 87.3%; Pred. No. 8.4e-70;
 Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 ETLPPKYLHYDPETGHOGLCDKCAPGTYLKHCHTVRRKTLCPDPSHYTSDSWHTSDDEV 60
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 22 etfppkylyhydeetshqllcdkcpptgylkqhctakwktvcapcpdhytswhtsdecl 81
 QY 61 YCSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFLKLRSCPPGSGVQAGTPERNTV 120
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 82 ycspvckelqsvkqecnrtnhrvcecegryleiefclkhscppgfgvvagqlperntv 141
 QY 121 CKKCPDGFSGSETSSKAPCIKHTNCGSTFGLLILQGNATHNNVCSGNREATOR 173
 ||||||| ||||||| ||||||| : ||: ||||| |||||||
 Db 142 ckrcpdgffsnetsskapeckrhncsvfgllllctqgnathndnlesgnsesctq 194

RESULT 7
 R99941
 ID R99941 standard; Protein; 327 AA.
 XX R99941;
 XX AC
 XX 23-APR-1997 (first entry)
 XX Mutated OCIF, OCIF-DDD2.
 XX DE
 XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
 XX osteoporosis.
 XX OS
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT

```

OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..21
FT /note= "Signal peptide"
FT 22..327
FT Protein /note= "Mature OCIF-DDD2"
FT Misc-difference 273..274
FT /note= "Position of deletion, delta 253-326"
XX
XX PN W09626217-A1.
XX PD 29-AUG-1996.
XX 20-FEB-1996; 96WO-JP00374.
XX 21-JUL-1995; 95JP-0207508.
XX 20-FEB-1995; 95JP-0054977.
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX WPI; 1996-402320/40.
XX DR N-PSDB; T33171.
XX
XX PT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX for bone resorption control, esp. treatment of osteoporosis
XX
XX PS Claim 59; Page 115-116; 183pp; Japanese.
XX
XX CC This sequence represents a mutated version of the full length
XX osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX sequence represents OCIF-DDD2 in which amino acids 253-326 of the
XX mature OCIF protein are deleted. The OCIF of the invention
XX has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX cation-exchangers or heparin and its activity is lowered after 10 mins
XX at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX deg.C. OCIF is useful in the control of bone resorption and therefore
XX in the treatment and prevention of disorders of bone resorption, e.g.
XX osteoporosis.
XX
XX SQ Sequence 327 AA;

```

```

Query Match 89.3%; Score 887; DB 17; Length 327;
Best Local Similarity 87.3%; Pred. No. 8.4e-70;
Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

```

```

QY 1 ETLPRKYLHYDEPTGHOILCDKCAPGTYLKQCHYVRKRLTCVPCPDHSTDSWHTSDDEV 60
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 22 etlppkylhydeetshqllcdkcpqpytlkqncakwktvcapcpdhytldswhtsdecl 81
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
QY 61 YCSPPCKELQSVKQECNFTNHNRCVCEEGRYLIEFCLKHRSCTPGSGVVOAGTPEERNV 120
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 82 ycsppckelqsvkqecnftnhnrvcecegryleiefclkhscppgfyvgagqperntlv 141
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
QY 121 CKKCPDGFSGTSSKAPCIKHTNCTFGLLDIQGNATHDNVCSGNREATOK 173
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 142 ckrcpdgffsnetsskaperkhtnctsvfgllltqkgnathdnicsgnesetck 194
   ||||||| ||||||| ||||||| : ||| ||||| |||||||

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```

RESULT 8
ID W83928 standard; Protein: 349 AA.
XX
AC W83928;
XX
DT 01-MAR-1999 (first entry)
XX
DE Human FTNMA-070 partial polypeptide.

```

```

XX XX FTNMA-070; human; neurological disorder; diagnosis; therapy.
XX KM Homo sapiens.
XX OS W09848051-A2.
XX PN 29-OCT-1998.
XX PD 17-APR-1998; 98WO-US07714.
XX PF 10-OCT-1997; 97US-0062017.
XX PR 18-APR-1997; 97US-0044746.
XX XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX PI Holtzman D, McCarthy SA;
XX DR WPI; 1999-024021/02.
XX DR N-PSDB; V69279.
XX
XX PS Disclosure; Fig 2; 127pp; English.
XX
XX CC This is the amino acid sequence of a partial human FTNMA-070
XX CC polypeptide, deduced from a partial cDNA (see V69279). Full-length
XX CC FTNMA-070 (see W83926) is claimed. It is a novel protein havin:
XX CC homology to tumour necrosis factor receptor. FTNMA-070 nucleic
XX CC acids and polypeptides of the invention are useful as modulating
XX CC agents in regulating a variety of cellular processes. They can be
XX CC used for identifying compounds which bind to or modulate the
XX CC activity of the polypeptides (claimed). They can also be used in
XX CC screening assays, detection assays (e.g. chromosomal mapping,
XX CC tissue typing, forensic biology), predictive medicine (e.g.
XX CC diagnostic assays, prognostic assays, monitoring clinical trials,
XX CC and pharmacogenomics), and methods of treatment (e.g. therapeutic
XX CC and prophylactic) e.g. for neurological disorders.
XX
XX SQ Sequence 349 AA;

```

```

Query Match 89.3%; Score 887; DB 20; Length 349;
Best Local Similarity 87.3%; Pred. No. 9e-70;
Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

```

```

QY 1 ETLPRKYLHYDEPTGHOILCDKCAPGTYLKQCHYVRKRLTCVPCPDHSTDSWHTSDDEV 60
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 44 etlppkylhydeetshqllcdkcpqpytlkqncakwktvcapcpdhytldswhtsdecl 100
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
QY 61 YCSPPCKELQSVKQECNFTNHNRCVCEEGRYLIEFCLKHRSCTPGSGVVOAGTPEERNV 120
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 104 ycsppckelqsvkqecnftnhnrvcecegryleiefclkhscppgfyvgagqperntlv 163
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
QY 121 CKKCPDGFSGTSSKAPCIKHTNCTFGLLDIQGNATHDNVCSGNREATOK 173
   ||||||| ||||||| ||||||| : ||| ||||| |||||||
DB 164 ckrcpdgffsnetsskaperkhtnctsvfgllltqkgnathdnicsgnesetck 216
   ||||||| ||||||| ||||||| : ||| ||||| |||||||

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```

RESULT 9
ID R99943 standard; Protein: 351 AA.
XX
AC R99943;
XX
DT 23-APR-1997 (first entry)
XX
DE Mutated OCIF, OCIF-CC.
XX
KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resor:
XX osteoporosis.

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XX OS Synthetic.
XX FT Key
XX FT Peptide
XX FT Protein
XX FT /note= "Signal peptide"
XX FT /note= "Mature OCIF-CC"
XX PN W09626217-A1.
XX PD 29-AUG-1996.
XX PF 20-FEB-1996; 96WO-JP00374.
XX PR 21-JUL-1995; 95JP-0207508.
XX PR 20-FEB-1995; 95JP-0054977.
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX DR WPI: 1996-402320/40.
XX DR N-PSDB: T33173.
XX PT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis
XX PS Claim 65; Page 119-121; 183pp; Japanese.
XX CC This sequence represents a mutated version of the full length
XX CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX CC sequence represents OCIF-CC in which amino acids 331-380 of the
XX CC mature OCIF protein are deleted. The OCIF of the invention
XX CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX CC cation-exchangers or heparin and its activity is lowered after 10 mins
XX CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX CC deg.C. OCIF is useful in the control of bone resorption and therefore
XX CC in the treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX CC
XX SQ Sequence 351 AA;
XX
XX Query Match 89.3%; Score 887; DB 17; Length 351;
XX Best Local Similarity 87.3%; Pred. No. 9, 1e-70;
XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 ETLPPKYLHYPDPETGHQLCDKCAPGTYLKQHCYVRRKTLCPGPDHSDSYDMSWHTSDECV 60
XX ||||||| 11 ||||||| ||||||| : ||| ||||| |||||||
XX Db 22 etfppkylyhyeeetshqldckcpptylkqhctakwktvcapcdhytidswhstdecl 81
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX QY 61 YCSPVCKELQSVKQECNRTNHRVCECEBGRYLETEFLKHKRSCPPSGGVVQAGTPERNV 120
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX Db 82 yspvckelqsvkqecnrtnhrvcecekgrylelefcikhsrccppgfgvvagtpernv 141
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX QY 121 CKKCPDGFSEGTSSKAPCIKHTNCSFGILLIOKGNATHDNVCSGNREAROK 173
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX Db 142 ckrpcdgflfnetsskpcrkhncsvfgyllltqkgnathdnicsgnsesctqk 194
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX
XX RESULT 10
XX R99924
XX ID R99924 standard; Protein; 380 AA.
XX
XX AC R99924;
XX XX
XX DT 22-APR-1997 (first entry)
XX XX
XX DE Mature osteoclastogenesis inhibitory factor.
XX XX

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XX KM Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX KM osteoporosis.
XX XX
XX OS Homo sapiens.
XX XX
XX PN W09626217-A1.
XX PD 29-AUG-1996.
XX PF 20-FEB-1996; 96WO-JP00374.
XX PR 21-JUL-1995; 95JP-0207508.
XX PR 20-FEB-1995; 95JP-0054977.
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX XX
XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX DR WPI: 1996-402320/40.
XX DR N-PSDB: T36685.
XX DR
XX XX
XX PT DNA encoding osteoclastogenesis inhibitory factor protein - usef
XX PT for bone resorption control, esp. treatment of osteoporosis
XX XX
XX PS Claim 6; Page 62-64; 183pp; Japanese.
XX CC This sequence represents the mature osteoclastogenesis inhibitory
XX CC factor (OCIF) of the invention. The OCIF has a molecular weight by
XX CC SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-
XX CC reducing conditions. The protein is adsorbed onto cation-exchangers
XX CC or heparin and its activity is lowered after 10 mins at 70 deg.C or
XX CC 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
XX CC useful in the control of bone resorption and therefore in the
XX CC treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX CC
XX SQ Sequence 380 AA;
XX
XX Query Match 89.3%; Score 887; DB 17; Length 380;
XX Best Local Similarity 87.3%; Pred. No. 9, 1e-70;
XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 ETLPPKYLHYPDPETGHQLCDKCAPGTYLKQHCYVRRKTLCPGPDHSDSYDMSWHTSDECV 60
XX ||||||| 11 ||||||| ||||||| : ||| ||||| |||||||
XX Db 1 etfppkylyhyeeetshqldckcpptylkqhctakwktvcapcdhytidswhstdecl 60
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX QY 61 YCSPVCKELQSVKQECNRTNHRVCECEBGRYLETEFLKHKRSCPPSGGVVQAGTPERNV 120
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX Db 61 yspvckelqsvkqecnrtnhrvcecekgrylelefcikhsrccppgfgvvagtpernv 120
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX QY 121 CKKCPDGFSEGTSSKAPCIKHTNCSFGILLIOKGNATHDNVCSGNREAROK 173
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX Db 121 ckrpcdgflfnetsskpcrkhncsvfgyllltqkgnathdnicsgnsesctqk 173
XX ||||||| 11 ||||||| ||||||| ||||||| ||||||| |||||||
XX
XX RESULT 11
XX R99357
XX ID R99357 standard; Protein; 390 AA.
XX
XX AC R99357;
XX XX
XX DT 05-MAY-1997 (first entry)
XX XX
XX DE Human tumour necrosis factor receptor.
XX XX
XX KM Tumour necrosis factor; TNF; receptor; TNF-beta; ligand; tumour;
XX KM differentiation; immune response; autoimmune disease; inflammation;
XX KM septic shock; graft-versus-host; apoptosis.
XX XX
XX OS Homo sapiens.
XX XX

```


FH	Key	Location/Qualifiers
FT	Peptide	1..21
FT		/label= sig_peptide
PX		
PN	W09628546-A1.	
PD	19-SEP-1996.	
PX		
PF	15-MAR-1995;	95WO-US03216.
PR	15-MAR-1995;	95WO-US03216.
PX	29-MAR-1995;	95ZA-0002587.
PA	(HUMA-) HUMAN GENOME SCL INC.	
XX	Fleischmann RD, Greene JM;	
DR	WPI: 1996-433821/43.	
DR	N-PDB: T35475.	
XX		
PT	New human tumour necrosis factor receptor - used to develop prods.	
PT	for treating e.g. tumours, infection, auto-immune disease, graft	
PT	rejection, cytotoxicity or inflammation	
PS	Claim 14; Fig 1; 59pp; English.	
XX		
CC	The receptor binds to TNF, and in particular, TNF-beta.	
CC	The receptor may be used for screening for antagonists and agonists	
CC	of the receptor and for ligands for the receptor. Such agonists may	
CC	be used to inhibit the growth of tumours, to stimulate cellular	
CC	differentiation, to mediate the immune response and anti-viral	
CC	response, to regulate growth and provide resistance to certain	
CC	infections. The antagonists may be used therapeutically, to treat	
CC	autoimmune diseases, inflammation, septic shock, to inhibit graft-	
CC	versus-host reactions, and to prevent apoptosis.	
XX		
SQ	Sequence 390 AA;	
	Query Match 89.3%; Score 887; DB 17; Length 390;	
	Best Local Similarity 87.3%; Pred. No. 1e-69;	
	Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;	
Dd	1 ETLPRKYLHYDEPETHQLLDCACAPGTYLKQHCTVRRKRLCVPCPDHSYTDTSWHTSDECY 60 : :	
Dd	22 elfppkyihydeetsahqllcdkcpptylkghtctakwktvcapcpdhyytidswhtsdecl 81	
Oy	61 YCSPPCKELQSKQCNCRTHNRNVCESCEGRYLEIEFCLKHRSCPGSGYVQAGTEBRNTV 120 	
Dd	82 ycsppckelqykqgcncrthnrvcceckegryleiefclkhrcspgfyvvgagteperntv 141 	
Oy	121 CKKCDDGFSSGTSKAPCIKHTNSTFGLLIIOGNATHDWCNSGNREATOK 173 	
Dd	142 ckrcpdgffsnetskapcrkhtnscsvigllltqkgnathdnicsgnesetqk 194	
RESULT 12		
ID W53238		
XX W53238 standard; Protein; 391 AA.		
AC W53238;		
XX		
DT 15-JUL-1998 (first entry)		
XX		
DE Human OCIF genome DNA-2 protein.		
XX		
KW Human; OCIF; genome; osteoclast; antihypretic; osteoporosis;		
KW rheumatism; multiple sclerosis.		
XX		
OS Homo sapiens.		
XX		
FN W09807840-A1.		
XX		

Query Match	Best Local Similarity	89.3%;	Score 887;	DB 19;	Length 391;
Matches 151;	Conservative 7;	Mismatches 15;	Indels 0;	Gaps 0;	
QY 1	ENTLPKRYLHYPERETHGHLCDCKACAGTYLKLQHCYVRKRTLYLPCPDHSHYTSMTNDS	1	0	0	
DB 12	ELFIPKRYLHYDEETSHGLLIDCKCPGTYLKLQHCIAKWKTCVACPDPDHYLTSWHS	1	0	0	
QY 61	YCSPYCKELOSQKOCNCFTHNVRCECEGRYLEIFCCKHRSQCPGSGVVOAGPPEKNTV	120			
DB 72	YCSPYCKEQLGYVKGCEMTLHNVCECKEGRYLEIFCCKHRSQCPGSGVVOAGPPEKNTV	131			
QY 121	CKKCGDFGFSGETSSKAPCIKHTNCSFTGGLLIDCKGNATHDNCVSGNEATOK	173			
DB 122	CKRCPDGFISNETSKAPCRKHTNCSFTGGLLIDCKGNATHDNCVSGNEATOK	184			
RESULT 13					
ID R99948					
AC R99948:					
XX 23-APR-1997	(first entry)				
XX DE	Mutated OCIF, OCIF-CBST.				
XX KW	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;				
XX RM	osteoporosis.				
XX OS	Synthetic.				
XX FT	Key				
XX FT	Peptide				
XX FT	Protein				

FT /note= "Mature OCIF-CBst"
 FT Misc-difference 392
 FT /label= Gln371Ileu
 XX
 XX WO9626217-A1.
 XX
 XX PD 29-AUG-1996.
 XX
 XX PF 20-FEB-1996; 96WO-JP00374.
 XX
 XX PR 21-JUL-1995; 95JP-0207508.
 XX 20-FEB-1995; 95JP-0054977.
 XX
 XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
 XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
 XX
 XX DR WPI; 1996-402320/40.
 XX
 XX N-PSDB; T33178.
 XX
 XX PT DNA encoding osteoclastogenesis inhibitory factor protein - useful
 XX for bone resorption control, esp. treatment of osteoporosis
 XX
 XX Claim 80; Page 126-128; 183pp; Japanese.
 XX
 XX This sequence represents a mutated version of the full length
 XX osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 XX sequence represents OCIF-CBst in which Gln 371 is substituted by
 XX Leu and amino acids 373-380 of the mature OCIF protein are deleted.
 XX These changes are caused by the introduction of a restriction site in
 XX the DNA encoding this protein. The OCIF of the invention has a
 XX molecular weight by SDS-PAGE of 60 kD under reducing conditions
 XX and 120 kD under non-reducing conditions. The protein is adsorbed onto
 XX cation-exchangers or heparin and its activity is lowered after 10 mins
 XX at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
 XX deg.C. OCIF is useful in the control of bone resorption and therefore
 XX in the treatment and prevention of disorders of bone resorption, e.g.
 XX osteoporosis.
 XX
 XX SO Sequence 393 AA:
 XX
 XX Query Match 89.3%; Score 887; DB 17; Length 393;
 XX Best Local Similarity 87.3%; Pred. No. 1e-69;
 XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 XX
 XX QY 1 ETLPKYLHDPETGHOILDKCAPGYTLKQHCYVRKRTLCVPPDHSDSYDMSWHTSDECV 60
 XX ||||||||| ||||||||| ||||||||| : ||: ||||| |||||||||
 XX Db 22 etfpkylhydeetsqllcdkcpptylkqhctakwkcvcapcdpyyidswhstdecl 81
 XX
 XX QY 61 YCSFVCKEIQSVKQECNRTNRRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERNV 120
 XX ||||||||| ||||||||| ||||||||| : ||||||||| |||||||||
 XX Db 82 ycsfvckelqyvgqecrtnrvceckegylelefclkrscppgfygvagtperntv 141
 XX
 XX QY 121 CKKCPDGFSGFSGTSSKAPCIKHTNCSFTFGLLLIQKGNAHDNWCNGNRATOK 173
 XX ||:||||||| ||||||||| ||||||||| ||||||||| |||||||||
 XX Db 142 ckrcpdgffsnetsskpcrkhnscvfglllctqgnathdnicsgnsestqk 194
 XX
 XX RESULT 14
 XX ID W57636 standard; Protein; 395 AA.
 XX
 XX AC W57636;
 XX
 XX XX 27-AUG-1998 (first entry)
 XX
 XX DE Modified TRI receptor protein.
 XX
 XX KW TRI receptor; tumour necrosis factor receptor-1; TNF-alpha; TNF-beta;
 XX inhibitor; tumour growth; tumour necrosis; microorganism infection;
 KW cellular differentiation stimulation; ionising radiation; septic shock;

KW anti-viral response; growth regulator; immune response; meningococemia;
 KW autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria;
 KW AIDS; therapy.
 XX
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO9812344-A1.
 XX
 XX XX 26-MAR-1998.
 XX
 XX XX 18-SEP-1996; 96WO-US15003.
 XX
 XX XX 18-SEP-1996; 96WO-US15003.
 XX
 XX XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX XX PI Fleischmann RD, Greene JM, Ni J;
 XX
 XX XX DR WPI; 1998-217278/19.
 XX
 XX XX N-PSDB; V24487.
 XX
 XX PT New isolated tumour necrosis factor receptor - useful for develop
 XX products for treating, e.g. tumours, auto-immune disease(s), graft
 XX rejection, apoptosis or inflammation
 XX
 XX Claim 13; Fig 2; 111pp; English.
 XX
 XX This sequence is a tumour necrosis factor receptor-1 (TRI) recei
 XX of the invention. The DNA can be used to produce a recombinant host
 XX cell by inserting it into a vector, which is then used to transfect the
 XX host cell. The TRI receptor can bind both TNF-alpha and TNF-beta. TRI
 XX receptor agonists can be used for inhibition of tumour growth an
 XX necrosis of tumours. They can also be used to stimulate cellular
 XX differentiation, e.g. T cell, fibroblasts or haematopoietic cell
 XX against microorganisms and prevent related disease. The agonists may
 XX also be used to protect against the deleterious effects of ionising
 XX radiation produced during a course of radiotherapy, e.g. denatur
 XX enzymes, lipid peroxidation or DNA damage. The agonists may further be
 XX used to mediate an anti-viral response, to regulate growth, to mediate
 XX the immune response and to treat immunodeficiencies related to diseases
 XX such as HIV. Antagonists to the TRI receptor may be used to treat
 XX autoimmune diseases, e.g. graft versus host rejection and allograft
 XX rejection, and T cell mediated autoimmune diseases. They may also be used
 XX to prevent apoptosis. They may also be used to prevent cytotoxicity and
 XX to treat septic shock, meningococemia, inflammation, bacterial
 XX infections, cachexia, cerebral malaria or AIDS. The products can also be
 XX used for diagnosing the above diseases.
 XX
 XX SO Sequence 395 AA:
 XX
 XX Query Match 89.3%; Score 887; DB 19; Length 395;
 XX Best Local Similarity 87.3%; Pred. No. 1e-69;
 XX Matches 151; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 XX
 XX QY 1 ETLPKYLHDPETGHOILDKCAPGYTLKQHCYVRKRTLCVPPDHSDSYDMSWHTSDECV 60
 XX ||||||||| ||||||||| ||||||||| : ||: ||||| |||||||||
 XX Db 22 etfpkylhydeetsqllcdkcpptylkqhctakwkcvcapcdpyyidswhstdecl 81
 XX
 XX QY 61 YCSFVCKEIQSVKQECNRTNRRVCECEGRYLEIEFCLKHSRCPGSGVVOAGTPERNV 120
 XX ||||||||| ||||||||| ||||||||| : ||||||||| |||||||||
 XX Db 82 ycsfvckelqyvgqecrtnrvceckegylelefclkrscppgfygvagtperntv 141
 XX
 XX QY 121 CKKCPDGFSGFSGTSSKAPCIKHTNCSFTFGLLLIQKGNAHDNWCNGNRATOK 173
 XX ||:||||||| ||||||||| ||||||||| ||||||||| |||||||||
 XX Db 142 ckrcpdgffsnetsskpcrkhnscvfglllctqgnathdnicsgnsestqk 194
 XX
 XX RESULT 15
 XX ID R99942 standard; Protein; 399 AA.
 XX

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:38 ; Search time 41.41 Seconds

(without alignments)
611.372 Million cell updates/sec

Title: US-09-389-545-2_COPY_186_401
Perfect score: 1113
Sequence: 1 SGNREATQKCIDVTLCEEA.....QKLFLEMIGNQVSKISCL 216

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-mammal:*
6: sp-invertebrate:*
7: sp-mhc:*
8: sp-organeller:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	401	11	008712
2	1069	96.0	401	11	008727
3	969	87.1	401	4	000300
4	938	84.3	372	4	090HP4
5	105	9.4	636	4	09NMX2
6	105	9.4	674	4	09P010
7	105	9.4	691	4	09POX5
8	105	9.4	694	4	09UKA1
9	103	9.3	731	4	095287
10	100	9.0	535	4	090UC8
11	96.5	8.7	690	4	090UT7
12	95	8.5	203	10	040767
13	95	8.5	486	5	019863
14	94	8.4	729	11	088317
15	94	8.4	729	11	090YE6
16	91.5	8.2	901	11	090ZJ4
17	91	8.2	1364	13	09YHY6
18	90.5	8.1	833	5	017102
19	90	8.1	1103	4	09NNY6

20	89.5	8.0	1232	4	09NY24	09ny24 h. sapien
21	89	8.0	888	5	09VDD8	09vdd8 d. rerio
22	88.5	8.0	184	10	09L198	09l198 h. sapien
23	88.5	8.0	469	5	09NSN7	09nsn7 h. sapien
24	88.5	8.0	585	4	090Q07	090q07 h. sapien
25	88.5	8.0	710	5	09XTS0	09xts0 caenorhabd
26	88.5	8.0	1388	13	091785	091785 xenopus lae
27	88	7.9	361	13	090608	090608 gallus gall
28	88	7.9	523	5	018378	018378 caenorhabd
29	88	7.9	1225	13	090640	090640 h. sapien
30	88	7.9	5293	5	09V6V2	09v6v2 d. rerio
31	88	7.9	5385	5	09V6V3	09v6v3 d. rerio
32	87	7.8	823	2	067119	067119 a. taen
33	87	7.8	1215	2	092771	092771 ch. trypa p
34	87	7.8	1215	2	09J5S9	09j5s9 ch. trypa p
35	87	7.8	4151	5	096936	096936 d. rerio
36	87	7.8	5201	5	090479	090479 d. rerio
37	86.5	7.8	1828	11	090YE3	090yf3 i. mus norv
38	86	7.7	706	2	09RP72	09rp72 p. cella
39	86	7.7	1442	2	09POB4	09pob4 u. ma
40	86	7.7	1837	3	074424	074424 sc. zosach
41	86	7.7	2871	4	014189	014189 h. sapien
42	86	7.7	2871	4	075993	075993 h. sapien
43	85.5	7.7	1360	13	09YGS5	09ygs5 a. mus lae
44	85	7.6	732	5	024557	024557 d. rerio
45	85	7.6	732	5	024558	024558 d. rerio

ALIGNMENTS

RESULT 1
ID 008712 PRELIMINARY; PRT: 401 AA.
AC 008712; 070202;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DR 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE OSTEOCALCIN PRECURSOR (OSTEOCALCINOGENESIS INHIBITORY FACTOR (OCIF)).
GN INFRSFILB OR OPG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosteo.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=KIDNEY;
RX MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shuman J., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattifony W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
RT Cell 89:309-319(1997).
RL (2)
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA, AND NIH SWISS;
RX MEDLINE=98382527; PubMed=9714833;
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morin Higashio K.;
RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
RT Gene 215:339-343(1998).
RL -I- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
CC -I- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94331; AAB53708.1; -.
 DR EMBL: AB013898; BAA28269.1; -.
 DR EMBL: AB013903; BAA33388.1; -.
 DR EMBL: AB013899; BAA33388.1; JOINED.
 DR EMBL: AB013900; BAA33388.1; JOINED.
 DR EMBL: AB013901; BAA33388.1; JOINED.
 DR EMBL: AB013902; BAA33388.1; JOINED.
 DR HSSP: P25942; ICDF.
 DR MGI: MGI:109587; OPG.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PIRAM: PR00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS0017; DEATH_DOMAIN; 1.
 DR PROSITE: PS0050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -. 1.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT CHAIN 1 21
 FT DOMAIN 22 401
 FT REPEAT 23 201
 FT REPEAT 23 201
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT REPEAT 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
 Query Match 100.0%; Score 1113; DB 11; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2e-80;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 181 RKTMRFLSHFTMYRKYOKLEFLEMIGNOVSKISCL 216
 DB 366 RKTMRFLSHFTMYRKYOKLEFLEMIGNOVSKISCL 401
 RESULT 2
 ID 008727 PRELIMINARY; PRT; 401 AA.
 AC 008727;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE OSTEOBLASTOGENESIS INHIBITORY FACTOR
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 OX NCBI_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luechly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimada
 RA Derose M., Elliott R., Colombo A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patt
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT *Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.;
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94330; AAB53707.1; -.
 DR HSSP: P25942; ICDF.
 DR INTERPRO: IPR001368; -.
 DR PIRAM: PR00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS0050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; -. 1.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT CHAIN 1 21
 FT DOMAIN 22 401
 FT REPEAT 23 201
 FT REPEAT 23 201
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT REPEAT 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31FD4E573A CRC64;
 Query Match 96.0%; Score 1069; DB 11; Length 401;
 Best Local Similarity 95.4%; Pred. No. 5.9e-77;

Matches 206; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 SGNREATORCGIDVTLCEAEFFRAVPTKIIPWLSVLDNPGTKVNAESVERIKRRH 60
 DB 186 SGNREATORCGIDVTLCEAEFFRAVPTKIIPWLSVLDNPGTKVNAESVERIKRRH 245
 OY 61 SOBQOTOLKLMKHONRDMYKIIODIDLCSSVORHGHNSLTTEOLALMESLPK 120
 DB 246 SOBQOTOLKLMKHONRDMYKIIODIDLCSSVORHGHNSLTTEOLALMESLPK 305
 OY 121 KISPEIERTKTKSSSEOLKLSLMRINKGDDTLKGLMALKLTKTSHPKTYTHSL 180
 DB 306 KISPEIERTKTKSSSEOLKLSLMRINKGDDTLKGLMALKLTKTSHPKTYTHSL 365
 DB 181 KRTMRFLHSTMYRLYOKLFLEMIGNOVOSVKISCL 216
 DB 366 KRTMRFLHSTMYRLYOKLFLEMIGNOVOSVKISCL 401

RESULT 3
 ID 000300 PRELIMINARY; PRT; 401 AA.
 AC 000300; 060236;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).
 GN TNFRSF1B OR OPG OR OCIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA *Osteoprotegerin: a novel secreted protein involved in the regulation
 RA of bone density.";
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG FIBROBLAST;
 RX MEDLINE=98151033; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RA *Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RA osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RA osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE=98351569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RA *Cloning and characterization of the gene encoding human
 RA osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, H.
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
 DR EMBL: AB002146; BAA25910.1;
 DR EMBL: AB008822; BAA32076.1;
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1;
 DR HSP; P25942; ICDF.
 DR MIM: 602643;
 DR INTERPRO: IPR001368;
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PRODOM: PD000771; 1.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 183 4 X TNFR-CYS.
 FT REPEAT 23 183 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 152 152 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
 SQ SEQUENCE 401 AA; 45996 MW; EB42FASIC9D7C7IE CRC64;

Query Match 87.1%; Score 969; DB 4; Length 401;
 Best Local Similarity 84.7%; Pred. No. 4.7e-69;
 Matches 183; Conservative 19; Mismatches 14; Indels 0;

OY 1 SGNREATORCGIDVTLCEAEFFRAVPTKIIPWLSVLDNPGTKVNAESVERIKRRH 60
 DB 186 SGNREATORCGIDVTLCEAEFFRAVPTKIIPWLSVLDNPGTKVNAESVERIKRRH 245
 OY 61 SOBQOTOLKLMKHONRDMYKIIODIDLCSSVORHGHNSLTTEOLALMESLPK 120
 DB 246 SOBQOTOLKLMKHONRDMYKIIODIDLCSSVORHGHNSLTTEOLALMESLPK 305
 OY 121 KISPEIERTKTKSSSEOLKLSLMRINKGDDTLKGLMALKLTKTSHPKTYTHSL 180
 DB 306 KISPEIERTKTKSSSEOLKLSLMRINKGDDTLKGLMALKLTKTSHPKTYTHSL 365
 OY 181 KRTMRFLHSTMYRLYOKLFLEMIGNOVOSVKISCL 216
 DB 366 KRTMRFLHSTMYRLYOKLFLEMIGNOVOSVKISCL 401

RESULT 4
 ID 090HP4 PRELIMINARY; PRT; 372 AA.
 AC 090HP4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE OSTEOPROTEGERIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL: AF134187; AAF20168.1; -.
DR HSSP: P25942; ICDF.
DR INTERPRO: IPR001368; -.
DR PFAM: PF00020; TNER_C6; 3.
DR PROSITE: PS00652; TNER_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNER_NGFR_2; 2.
FT NON_TER 1
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CD3 CRC64;

Query Match 84.3%; Score 938; DB 4; Length 372;
Best Local Similarity 84.6%; Pred. No. 1,2e-66;
Matches 176; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

OY 1 SGNRATGCGIDVTLCGEAFRFAVPKTIIPNMTSVLDSPGKVAESVERIKRRHS 60
DB 165 SGNSESTGCGIDVTLCGEAFRFAVPKTIIPNMTSVLDSPGKVAESVERIKRRHS 224
61 SGEQTFOLKLKMHONRDQEMVKIIOIDIDLCSSVQRHLSHNLTTQDLALMESLPK 120
DB 225 SGEQTFOLKLKMHONRDQEMVKIIOIDIDLCSSVQRHLSHNLTTQDLALMESLPK 284
OY 121 KISPEIERTRKTCSSSEQLKLKSLMRKNGDDOTLKGMLAKHLKTSHPKTVTSHL 180
DB 285 KVGADIDIKTKKACRPSDIIKLKSLMRKNGDDOTLKGMLAKHLKTSHPKTVTSHL 344
OY 181 RRTMRFLSHFTMYRLYOKLFLEMIGNOV 208
DB 345 KTIIRFLSHFTMYRLYOKLFLEMIGNOV 372

RESULT 5
O9NMX2 PRELIMINARY; PRT; 636 AA.
AC O9NMX2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CDNA FLJ20146 FIS. CLONE COL07877.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Kawabata A., Hiki J., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RT Okitani R., Ota T., Suzuki Y., Oiyashi M., Nishi T., Shibahara T.,
RT Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK000153; BAA90978.1; -.
SQ SEQUENCE 636 AA; 72098 MW; B541A0C9E8DFBAF CRC64;

Query Match 9.4%; Score 105; DB 4; Length 636;
Best Local Similarity 26.3%; Pred. No. 1.6;
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSQOTFOLK---LMKHONRDQEMVKIIOIDIDLCSSVQRH-IG 101
DB 90 EELDKIKKVIAGHOSQKDTAELLGLSLMWAHERQKFFKYSVDEKDKAEVSEHSTG 149
102 HSNLTTEQLALMESLPKTKISPEIERTRKTCSSSEQLKLKSLMRKNGDDOTLKGML 161
DB 150 ITHLPPEVMTLSIFSYL-----NPELRCRCQSVSMKWSOLTTGTGSLW----- 190

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OY 162 YALKHKTSHPK 174
DB 191 ---KHLVPVHMAR 200

RESULT 6
O9P010 PRELIMINARY; PRT; 674 AA.
AC O9P010;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE P45KP2-LIKE PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Jin Y., Jiang C., Li
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in the human adrenal gland.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Ren S., Shi J., Huang C., Jiang C., Li Y., Zhou J., Yu Y., Xu
RA Wang Y., Fu G., Chen Z., Han Z.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157323; AAF67489.1; -.
SQ SEQUENCE 674 AA; 76543 MW; 7B75B339DE70E7FC CRC64;

Query Match 9.4%; Score 105; DB 4; Length 674;
Best Local Similarity 26.3%; Pred. No. 1.7;
Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSQOTFOLK---LMKHONRDQEMVKIIOIDIDLCSSVQRH-IG 101
DB 128 EELDKIKKVIAGHOSQKDTAELLGLSLMWAHERQKFFKYSVDEKDKAEVSEHSTG 149
102 HSNLTTEQLALMESLPKTKISPEIERTRKTCSSSEQLKLKSLMRKNGDDOTLKGML 161
DB 188 ITHLPPEVMTLSIFSYL-----NPELRCRCQSVSMKWSOLTTGTGSLW----- 228
OY 162 YALKHKTSHPK 174
DB 229 ---KHLVPVHMAR 238

RESULT 7
O9P0X5 PRELIMINARY; PRT; 691 AA.
AC O9P0X5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE F-BOX PROTEIN FLR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Shibahara N.;
RT "cDNA cloning of a new human protein, FLR1, containing both mol
RT F-box and leucine-rich repeat.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF142481; AAF66616.1; -.
SQ SEQUENCE 691 AA; 78554 MW; 923A1B31590E5145 CRC64;

```


Query Match 9.4%; Score 105; DB 4; Length 691;
 Best Local Similarity 26.3%; Pred. No. 1.7;
 Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSOEFOFLK---LMKHQNRDQEWKTIIDIDLCSSVORH-IG 101
 DB 145 EEKLDIKKKYIAOHCOSKDTAEILRGISLWNNHAEEROKFKYVSDEKSDKEAEVSEHSTG 204
 OY 102 HSNLITTEQLALMESLPGRKISPEIERFRKTKSSPOLKLSLWRKNGDODTLKGLM 161
 DB 205 ITHLPPEVMSIFSYL-----NPQELCRCSQVSMKMSQLTKTGSIM----- 245
 OY 162 YALKHLKTSHPK 174
 DB 246 ---KHLYPVHMAR 255

RESULT 8
 ID 09UKA1 PRELIMINARY; PRT; 694 AA.
 AC 09UKA1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE F-BOX PROTEIN FBL5 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Winston J.T., Elledge S.J., Harper W.;
 RT "A family of mammalian F-box proteins."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF176700; AAF03700.1;
 DR INTERPRO: IPR001611;
 DR INTERPRO: IPR001810;
 DR PFAM: PF00560; LRR: 1.
 DR PFAM: PF00646; F-box; 1.
 FT NON_TER
 SQ SEQUENCE 694 AA; 78795 MW; 198D1FE13F95BC68 CRC64;

Query Match 9.4%; Score 105; DB 4; Length 694;
 Best Local Similarity 26.3%; Pred. No. 1.7;
 Matches 35; Conservative 22; Mismatches 46; Indels 30; Gaps 5;

OY 50 ESVERIKRR---HSSOEFOFLK---LMKHQNRDQEWKTIIDIDLCSSVORH-IG 101
 DB 148 EEKLDIKKKYIAOHCOSKDTAEILRGISLWNNHAEEROKFKYVSDEKSDKEAEVSEHSTG 207
 OY 102 HSNLITTEQLALMESLPGRKISPEIERFRKTKSSPOLKLSLWRKNGDODTLKGLM 161
 DB 208 ITHLPPEVMSIFSYL-----NPQELCRCSQVSMKMSQLTKTGSIM----- 248
 OY 162 YALKHLKTSHPK 174
 DB 249 ---KHLYPVHMAR 255

RESULT 9
 ID 095287 PRELIMINARY; PRT; 731 AA.
 AC 095287;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE GOLGIN-84.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-TESTIS;
 RX MEDLINE=99-15642; PubMed=9915833;
 RA Bascom R.A., Srinivasan S., Nussbaum R.L.;
 RT "Identification and characterization of golgin-84, a novel Golgi
 integral membrane protein with a cytoplasmic coiled-coil domain."
 RL J. Biol. Chem. 274:2953-2962(1999).
 DR EMBL; AF085199; AAD09753.1;
 SQ SEQUENCE 731 AA; 82990 MW; E708D023C60B02BA CRC64;

Query Match 9.3%; Score 103; DB 4; Length 731;
 Best Local Similarity 23.5%; Pred. No. 2.6;
 Matches 39; Conservative 36; Mismatches 75; Indels 16; Gaps 5;

OY 49 AESVERIKRRHSSOEFOFLKLMK---HQRDQEWKTIIDIDLCSSVORHSGN-IG 106
 DB 463 ASMELEELRHEKMGREELQKLMGQIHQARSE-----LQDME-----AQVNAEESA 510
 OY 107 TEQLALMESLPGRKISPEIERFRKTKSSPOLKLSLWRKNGDODTLKGLMAYALK-IG 5
 DB 511 REQLDLDHQAQKASKOLETELEKOEFEYIE-EDLYRTKNTLOSRIKDRDEI-IG 369
 OY 167 LKTSHPKTYTHSLRKTW-RFLHSFTMYRLYOKLFLPMIGNQVSY 211
 DB 570 LRNQLTKTILSSQSELENRLHQLTETTLIQKOTMLESSTENSL 615

RESULT 10
 ID 09UKC8 PRELIMINARY; PRT; 535 AA.
 AC 09UKC8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE F-BOX PROTEIN FBL5 (FRAGMENT).
 GN FBL5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cenciarelli C., Chaiur D.S., Guardavaccaro D., Parks W., Vidal M.
 RA Pagano M.;
 RT "Identification of a family of human F-box proteins."
 RL Curr. Biol. 9:1177-1179(1999).
 DR EMBL; AF174591; AAF04512.1;
 DR INTERPRO: IPR001611;
 DR INTERPRO: IPR001810;
 DR PFAM: PF00560; LRR: 1.
 DR PFAM: PF00646; F-box; 1.
 FT NON_TER
 SQ SEQUENCE 535 AA; 59824 MW; 110B59DF98C3F1EE CRC64;

Query Match 9.0%; Score 100; DB 4; Length 535;
 Best Local Similarity 26.4%; Pred. No. 3.2;
 Matches 32; Conservative 19; Mismatches 44; Indels 26; Gaps 4;

OY 58 RHSSOEFTPOLK---LMKHQNRDQEWKTIIDIDLCSSVORH-LGHSNLTTEQL-IG 113
 DB 1 OHOSQKTAELKGLSLWNNHAEEROKFKYVSDEKSDKEAEVSEHSTGTHLPPEVMSL-IG 60
 OY 114 MESLPGRKISPEIERFRKTKSSPOLKLSLWRKNGDODTLKGLMAYALKHLKTSHP-IG 173
 DB 61 FSYL-----NPQELCRCSQVSMKMSQLTKTGSIM-----KHLYPVHMAR 98
 OY 174 K 174
 DB 99 R 99

```

Query Match      8.7%; Score 96.5; DB 4; Length 690;
Best Local Similarity 26.3%; Pred No. 8.1;
Matches 35; Conservative 22; Mismatches 45; Indels 31; Gaps 6

QY 50 ESVERIKRR---HSSOEOTFOLK---LWKQNNDQEWK-KITIDIDICSSVRHGLG 101
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 ELKRIKKKVIYAQHCSQNDTALLGLSLMNNAEERQKFKSYVDKSKAEYS-ETHSG 203
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 102 HSNLTBOLLAMESLPCKGISPEEIERTRKTCSSQEDLLKLTLWRIKNGDDTLKGLM 161
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 204 ITHLPPEYMLSTFSTYL-----NPQELCRSQYSMKMSQLTKTGSLM----- 244
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 162 YALKHLKTSHEPK 174
   |||||::|::|
Db 245 ---KHLVPVHMAR 254

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[illegible]

Db 277 SKKKEAIRN-----VKKLVDTYNTVTRMQRKRVCTSPLEEEAVALARDLDSTTEEFL 332
 QY 118 PGKKISPEELER-----TRKCKSSBOLLKLSLMRK-MGDODTLG--- 159
 Db 333 PIDAIEMLEMEKLFNNKNDICRLIKNTKNTTTRVRIKTLFVROPKITGKREKLGNSL 392
 QY 160 -LWYALKHLKTSHF--PKVTYHSLRKTRMRLHSTFMYRLYOKL 199
 Db 393 DLSYHNFSLTTHGFGHPNSLSH-----YRSTOKI 421

RESULT 14

088317 PRELIMINARY; PRT; 729 AA.

Db 088317;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE RET-II PROTEIN.
 GN GOLGA5 OR RET-II.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=WHOLE BRAIN;
 RA Snider J., Sano H., Ohta M.;
 RT "Unknown, 5' similar to RET-II mRNA."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016784; BAA33010.1;
 DR MGI; MGI:1351475; G019a5.
 SQ SEQUENCE 729 AA; 82367 MW; 8418BEBE6E4865E1 CRC64;

Query Match 8.4%; Score 94; DB 11; Length 729;
 Best Local Similarity 22.3%; Pred. No. 14;
 Matches 37; Conservative 37; Mismatches 76; Indels 16; Gaps 5;

QY 49 AESVERIKRRHSQEQTFOLKLM--KHONROEMVKKIIDIDCESSVQRHLGSHNLT 106
 Db 461 ASSMELEELRHEKEMQKEETOKLMGOMHOLRSE-----LQDME-----AQOVSEASA 508
 Db 107 TEQLLALMESLPQKKISPEIERTRKCKSSBOLLKLSLMRKMGDODTLGIMYALKH 166
 Db 509 REQLDLODQIAKQRTSKQELTELERMKOEFRYME-EDLHRTKNTLQSRIRKDREREIOR 567
 QY 167 LKTSHPKTVTHSLRKTRMF-LHSFTMYRLYOKLFLEMIGNOVSY 211
 Db 568 LRNQLNKTLSNSSOSELSRLHQLTEFLIQTMTLESISTEKNSL 613

RESULT 15

090Y6 PRELIMINARY; PRT; 729 AA.

AC 090Y6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SUMIKO.
 GN SUMIKO.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ku P.T., You M.J., Cottam M.K., Bose H.R., Jr.;
 RT "Suppression of Anti-Immunoglobulin-Induced Apoptosis in B Lymphoma
 Cells by a Novel Nuclear Protein."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026274; AAF21628.1;

SQ SEQUENCE 729 AA; 82450 MW; 6E3389FA82361AFA CRC64;

Query Match 8.4%; Score 94; DB 11; Length 729;
 Best Local Similarity 22.3%; Pred. No. 14;
 Matches 37; Conservative 37; Mismatches 76; Indels 16; Gaps 5;

QY 49 AESVERIKRRHSQEQTFOLKLM--KHONROEMVKKIIDIDCESSVQRHLGSHNLT 106
 Db 461 ASSMELEELRHEKEMQKEETOKLMGOMHOLRSE-----LQDME-----AQOVSEASA 508
 Db 107 TEQLLALMESLPQKKISPEIERTRKCKSSBOLLKLSLMRKMGDODTLGIMYALKH 166
 Db 509 REQLDLODQIAKQRTSKQELTELERMKOEFRYME-EDLHRTKNTLQSRIRKDREREIOR 567
 QY 167 LKTSHPKTVTHSLRKTRMF-LHSFTMYRLYOKLFLEMIGNOVSY 211
 Db 568 LRNQLNKTLSNSSOSELSRLHQLTEFLIQTMTLESISTEKNSL 613

Search completed: January 27, 2001, 11:24:32
 Job time: 114 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:38 ; Search time 17.62 Seconds

(without alignments)
395.887 Million cell updates/sec

Title: US-09-389-545-2_COPY_186_401
Perfect score: 1113
Sequence: 1 SGNREARQKCGIDVTLCEFA.....OKLFLEMIGNQGVSKISCL 216

Working table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	9.0	1574	1	MYS2_YEAST
2	95.5	8.6	697	1	YESC_SCHPO
3	92	8.3	1309	1	ST16_SCHPO
4	91.5	8.2	1208	1	YDH6_SCHPO
5	90	8.1	463	1	DNAA_RICPR
6	88	7.9	3210	1	CEMF_HUMAN
7	87.5	7.9	1007	1	RGAL1_YEAST
8	86.5	7.8	1142	1	GIN4_YEAST
9	86	7.7	1752	1	DESP_HUMAN
10	84.5	7.6	229	1	SVAG_BACSV
11	83.5	7.5	1853	1	MYS2_YEAST
12	83	7.5	1230	1	SMC3_YEAST
13	83	7.5	1251	1	RBP2_PLAYB
14	83	7.5	1920	1	PCNT_MOUSE
15	83	7.4	3712	1	ACVS_CEPAC
16	82.5	7.4	1232	1	KIF4_HUMAN
17	82	7.4	1539	1	Y373_HUMAN
18	81.5	7.3	395	1	NUSA_HELPR
19	81.5	7.3	877	1	STR_RICPR
20	81.5	7.3	885	1	ASE1_YEAST
21	81.5	7.3	1032	1	KINN_HUMAN
22	81.5	7.3	1274	1	BXC_CLOBO
23	81	7.3	276	1	PANC_HELPJ
24	81	7.3	960	1	FGD1_MOUSE
25	80.5	7.2	1085	1	CNT7_SCHPO
26	80	7.2	1199	1	VNSC_P13H4
27	80	7.2	1129	1	JAK2_MOUSE
28	80	7.2	1132	1	JAK2_RAT
29	80	7.2	1636	1	BUD3_YEAST
30	79.5	7.1	350	1	GAL1_THEMA
31	79.5	7.1	1972	1	MST1_RABIT
32	79.5	7.1	2663	1	CEME_HUMAN
33	79	7.1	679	1	YIS3_YEAST

34	79	7.1	702	1	KFA3_HUMAN	O9Y496 huc saplen
35	79	7.1	961	1	FGD1_HUMAN	P88174 huc saplen
36	79	7.1	1132	1	DNBI_HSV6U	P52338 huc saplen
37	79	7.1	1132	1	DNBI_HSV6Z	P52338 huc saplen
38	79	7.1	1231	1	KIF4_MOUSE	P33174 huc saplen
39	79	7.1	2413	1	PR08_YEAST	P33334 huc saplen
40	79	7.1	2649	1	BPAL_HUMAN	O03001 huc saplen
41	78.5	7.1	710	1	Y026_YEAST	P39744 huc saplen
42	78.5	7.1	1027	1	KINN_MOUSE	O92219 huc saplen
43	78	7.0	563	1	ENV_BAEVM	P10269 huc saplen
44	78	7.0	782	1	BICD_DROME	P16568 huc saplen
45	78	7.0	979	1	T111_SCHPO	O09813 huc saplen

ALIGNMENTS

RESULT 1
ID ID MY52_YEAST STANDARD: PRT: 1574 AA.
AC P19524
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MYOSIN-2 ISOFORM.
GN MYO2 OR CDC66 OR YOR326W OR O6167.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetia.
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GFP88:
RX MEDLINE-91201404; PubMed-2016335.
RA Johnston G.C., Pendergast J.A., Singer R.A.:
RT "The Saccharomyces cerevisiae MYO2 gene encodes an essential myo-
RL for vectorial transport of vesicles." J. Cell Biol. 113:539-551(1991).
RN [2]
RP SEQUENCE OF 1-748 FROM N.A.
RC STRAIN-S288C / FY1679:
RX MEDLINE-97051589; PubMed-8896266;
RA Pearson B.M., Hernandez Y., Payne J., Wolf S.S., Kalogeropoulos A.
RT Schweizer M.:
RT "Sequencing of a 35.71 kb DNA segment on the right arm of yeast
RT chromosome XV reveals regions of similarity to chromosomes I and
RT XII." Yeast 12:1021-1031(1996).
RN [3]
RP SEQUENCE OF 677-1574 FROM N.A.
RX MEDLINE-97051586; PubMed-8896263;
RA Parle-Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.:
RT "Sequence of 29 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I." Yeast 12:999-1004(1996).
CC -!- FUNCTION: ESSENTIAL MYOSIN FOR VECTORIAL TRANSPORT OF VESIC-
CC PLAYS A DETERMINANT ROLE IN THE SPATIAL REGULATION OF BUD
CC FORMATION.
CC -!- SUBUNIT: MAY SELF-ASSOCIATE.
CC -!- MISCELLANEOUS: CA(2+) MAY PLAY A ROLE IN MYO2 ACTIVITY.
CC -!- SIMILARITY: BELONGS TO CLASS-5 MYOSINS. STRONGEST, TO YEAST MYO4.
CC
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CC EMBL: M35532; AAA34810.1; -
CC EMBL: X90565; CAA62184.1; -
CC EMBL: Z49821; CAA89973.1; -

CC EMBL: AJ223984; CAAL1758.1; -
 DR EMBL: 254140; CA90815.1; -
 KM Transmembrane; Meiosis.
 FT TRANSMEM 285 305 POTENTIAL.
 FT TRANSMEM 392 412 POTENTIAL.
 FT TRANSMEM 504 524 POTENTIAL.
 FT TRANSMEM 564 584 POTENTIAL.
 FT TRANSMEM 926 946 POTENTIAL.
 FT TRANSMEM 964 1004 POTENTIAL.
 SQ SEQUENCE 1309 AA; 147412 MW; 33EEA6794DBC6A82 CRC64;

Query Match 8.3%; Score 92; DB 1; Length 1309;
 Best Local Similarity 24.5%; Pred. No. 9.5;
 Matches 57; Conservative 31; Mismatches 77; Indels 68; Gaps 11;

QY 1 SCGNREATORCGIDVTLCEFAFFRAVPTKIIPMLSVLVSLP-----G 44
 DB 591 SASRKATYLLGEVLRLSDE-----LPIHLGAKIQSLPSLFNMAQFTAEPRVA 640
 QY 45 TKV--NAESVERIKRRHSQ--EQTFOLKLMKHQ-----NRDOENVK-KTIODID- 90
 DB 641 TSVLOSIESLNRKFSATQPSQTSLSL--LFKEQKTDGSEFRGQREHVKLMGQIJD 698
 QY 91 -----LCSSVORHGHGSLTTEOLLALMESLPKKISPEEIERKTKCKSSQLL---- 141
 DB 699 SHFRSLAETNVLATKNYOKRMWDLVQIME--GILLSPKRIDELTKTKERRLAIFY 755
 QY 142 -----KLISLMRIKNGDQ-----DTLKGIMVALKHLKTSHPKTYVHSL 180
 DB 756 KPFSNFFSIQNTKPKQKFIKVGCLFRTLLANPEGVKYLSEKVIKQIAESL 808

RESULT 4
 YDH6_SCHPO
 ID YDH6_SCHPO STANDARD: PRT; 1208 AA.
 AC 092351:
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DE HYPOTHETICAL 140.8 KDA PROTEIN C6G9.06C IN CHROMOSOME 1.
 NC SPAC6G9.06C.
 CC Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 CC Schizosaccharomycetaceae; Schizosaccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972:
 RA Murphy L., Harris D., Barrell B.G., Rajandream M.A., Connor R.E.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.

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CC EMBL: 281317; CAB03608.1; -
 DR Hypothetical protein; Coiled coil.
 FT DOMAIN 151 375 COILED COIL (POTENTIAL).
 FT DOMAIN 387 803 COILED COIL (POTENTIAL).
 FT DOMAIN 874 1091 COILED COIL (POTENTIAL).
 FT DOMAIN 1177 1204 COILED COIL (POTENTIAL).
 SQ SEQUENCE 1208 AA; 140763 MW; 70264159ADD42424 CRC64;

Query Match 8.2%; Score 91.5; DB 1; Length 1208;
 Best Local Similarity 25.0%; Pred. No. 9.5;
 Matches 54; Conservative 32; Mismatches 67; Indels 63; Gaps 11;

QY 34 WL-----SVLVSLPPTKVAESVERIKRRHSQEQTFOLKLMKHONRDOENVKLIK.
 DB 967 WLERSSTILDELESYRSQFNQON-----NLVQDNLEERLKEIQV----- 1011
 QY 90 DLCESSV--QRHLGSHNLTE--QLALMESLPCKKISPEE-----IERTRTCKSSQV 140
 DB 1012 EYVNNHFMQAEIEMNSVNTDEQMLKTRALQSTNNIDHLSLTLENRRKYS-- 1057
 QY 141 LKLSLM-----RIKNGDQD-----LGLMTALKHLKTSHPKTYVHSLKRT 183
 DB 1068 --LDDYNOIARARYKNLQSTQSGQYSEIEIGLSKTYLQSKCRRE--HSLK 1122
 QY 184 MRLHSE-----TWYRLQKLFLEMIGNOVQVKIS 214
 DB 1123 LAFSKRFILMLQGYETCKNLRLML---OKIGIS 1154

RESULT 5
 DNA_RICPR
 ID DNA_RICPR STANDARD: PRT; 463 AA.
 AC 059758:
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA.
 GN DNAA OR REP601.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RX MEDLINE-98442214; PubMed-9770078;
 RA Waite R.T., Shaw E.I., Winkler H.H., Wood D.O.;
 RT "Isolation and characterization of the dnaA gene of Rickettsia
 RT prowazekii.";
 RL Acta Virol. 42:95-101 (1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RX MEDLINE-99039499; PubMed-9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.H.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140 (1998).
 CC - FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REPLIC
 CC OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICAT
 CC IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS
 CC (DNAA BOX): 5'-TTATC(C/A)A(C/A)-3'. DNAA BINDS TO ATP AND 1

CC - SIMILARITY: BELONGS TO THE DNAA FAMILY.
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 CC or send an email to license@isb-sib.ch).

CC EMBL: U55213; AAA99160.1; -
 DR EMBL: AJ235272; CAAL5045.1; -
 DR INTERPRO: IPR001957; -
 DR PFAM: PF00308; bac_dnaA; 1.
 DR PRINTS: PR00051; DNAA.
 DR PROSITE: PS01008; DNAA; 1.
 KW DNA replication; DNA-binding; ATP-binding.
 FT NP_BIND 168 175 ATP (POTENTIAL).
 SQ SEQUENCE 463 AA; 53005 MW; F3CA5683DD3B1A1 CRC64;

Query Match 8.18; Score 90; DB 1; Length 463;
 Best Local Similarity 23.88; Pred. No. 3.9;
 Matches 49; Conservative 36; Mismatches 61; Indels 60; Gaps 12;

10 CGIVTLCDEAFRRVAFPKIIPNLVSV--DSIPGKVAESVERIKR-----58
 237 CGKSTO-EEFPHF--NTLIDNRQVISCDSRPSLDNIE--DRKISRIGMGLVADV 290

59 HSOEOTFOLKMKHNRDQEM-----VKRIIDIDCESSVOHILGSHMT 106
 291 HST--TTE-LRGLLEKIEQMANKIKVDYINFLASKIVSNRLEAGALKVIAHSMFT 346

107 TEOLIALESPLPKKISPEIER-TRTKCKSSQDL-----KLSIMRIKMGDQTLK 158
 347 L-----KAITLNTONILRDLRSNERITVEDIOKVAASRYNIKLSD-----389

159 GLMYALKHLKTSHPKTYTHSLRKTM 184
 390 --MYSRRLREVAPRQIATMYLSKTL 413

RESULT 6
 CENF_HUMAN STANDARD; PRT; 3210 AA.
 P49454: Q13246; Q13171;
 01-FEB-1996 (Rel. 33, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 CENP-F KINETOCHORE PROTEIN (CENTROMERE PROTEIN F) (MITOSIN) (AH ANTIGEN).
 CN CENP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 [1]
 [1] SEQUENCE FROM N.A.
 RC TISSUE-BREAST CARCINOMA;
 RX MEDLINE=95346175; PubMed=7542657;
 RA Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
 RT "CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";
 RL J. Cell Biol. 130:507-518(1995).
 [2]
 [2] SEQUENCE OF 1-1493 AND 1590-3210 FROM N.A.
 RX MEDLINE=95379848; PubMed=7651420;
 RA Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Jones D., Yang-Feng T.L., Lee W.-H.;
 RT "Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression.";
 RL Mol. Cell. Biol. 15:5017-5029(1995).
 [3]
 [3] SEQUENCE OF 2194-3210 FROM N.A.
 RX MEDLINE=95336446; PubMed=7612011;
 RA Li Q., Ke Y., Karp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
 RT "A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for nuclear localization.";
 RL Biochem. Biophys. Res. Commun. 212:220-228(1995).
 [4]
 [4] CHARACTERIZATION.
 RP MEDLINE=95370296; PubMed=7642639;
 RA Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;
 RT "The C terminus of mitotin is essential for its nuclear localization, centromere/kinetochore targeting, and dimerization.";
 RL J. Biol. Chem. 270:19545-19550(1995).
 [5]
 [5] CHARACTERIZATION.
 RP MEDLINE=98437347; PubMed=9763420;
 RA Chan G.K.T., Schaaf B.T., Yen T.J.;
 RT "Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBR1.";
 RL J. Cell Biol. 143:49-63(1998).
 CC -1- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH

CC RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBR1.
 CC -1- SUBUNIT: HOMO- OR HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS).
 CC REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.
 CC -1- DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
 CC -1- PTM: HYPERPHOSPHORYLATED DURING MITOSIS.
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DR EMBL; U19769; AAA82889.1; -;
 DR EMBL; U30872; AAA82935.1; -;
 DR EMBL; U25725; AAA86889.1; -;
 DR HSSP; P02649; ILE4.
 DR MIM; 600236; -;
 KW Mitosis; Phosphorylation; Antigen; Cell cycle.
 KM Chromosomal protein; Nuclear protein; Centromere; Coiled coil;
 FT DOMAIN 14 197
 FT DOMAIN 273 769
 FT DOMAIN 823 1328
 FT DOMAIN 1642 1746
 FT DOMAIN 1862 2987
 FT DOMAIN 2207 2568
 FT REPEAT 2207 2386
 FT REPEAT 2389 2568
 FT SITE 3015 3032
 FT CONFLICT 16 16
 FT CONFLICT 250 250
 FT CONFLICT 272 272
 FT CONFLICT 611 611
 FT CONFLICT 1494 1589
 FT CONFLICT 1611 1611
 FT CONFLICT 1811 1811
 FT CONFLICT 2242 2243
 FT CONFLICT 2335 2335
 FT CONFLICT 2492 2492
 FT CONFLICT 2545 2561
 SQ SEQUENCE 3210 AA; 367589 MW; 11D83324960E4334 CRC64;

Query Match 7.98; Score 88; DB 1; Length 3210;
 Best Local Similarity 23.48; Pred. No. 59;
 Matches 40; Conservative 34; Mismatches 55; Indels 42; Gaps 9;

50 ESVRIKRRHSSQETQFL-----KIMKHNRD-----QENVKI-----101-88
 2618 EISRILKQIDQDQVSKISQVGEHQMLKEQVLELRNLTVLEQKIQVLOQSNASLD 2677

89 -IDCESSVQVRLHLSNLTTEOLIALMESLPKKSISPEIER-----TRTKCKSSQDLK 42
 2678 TLEVLOQSYKYLENELTITKDKKSFVEKVKMIAKTELEQREHMAQTALEQEL- 2735

143 LLSLMRIKMGDQTLK- LMYALKHLKTSHP- KTVT--HSLKTRMFLH 188
 2736 -----SGEKRLAGELQLLEIRKSKQDLKELTLENSELRKSDCMH 2778

RESULT 7
 RGAL_YEAST STANDARD; PRT; 1007 AA.
 AC P39083; P39934;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE RHO-TYPE GTPASE ACTIVATING PROTEIN RGAL/DBM1.
 GN RGAL OR DBM1 OR THE1 OR YOR127W OR O3290 OR YOR3290W.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.
 RC STRAIN-S288C;
 RX MEDLINE-96239492; PubMed-8657111;
 RA Chen G.-C., Zheng L., Chan C.S.M.;
 RT "The LIM domain-containing Dbp1 GTPase-activating protein is required
 RT for normal cellular morphogenesis in Saccharomyces cerevisiae.";
 RL Mol. Cell. Biol. 16:1376-1390(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / FY1679;
 RX MEDLINE-97060020; PubMed-8904341;
 RA Wiemann S., Rechmann S., Benes V., Voss H., Schwager C., Vleck C.,
 RT Stegmann J., Zimmermann J., Ertle H., Paces V., Ansoerge W.;
 RT "Sequencing and analysis of 51 kb on the right arm of chromosome XV
 RT from Saccharomyces cerevisiae reveals 30 open reading frames.";
 RL Yeast 12:281-288(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97344368; PubMed-9200815;
 RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
 RA Schwager C., Paces V., Sander C., Ansoerge W.;
 RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
 RL Yeast 13:655-672(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE-96101594; PubMed-7498791;
 RA Stevenson B.J., Ferguson B., de Vargillo C., Bl E., Pringle J.R.,
 RA Amerer G., Sprague G.F. Jr.;
 RT "Mutation of Rga1, which encodes a putative GTPase-activating protein
 RT for the polarity establishment protein Cdc42p, activates the
 RT phenomene-response pathway in the yeast Saccharomyces cerevisiae.";
 RL Genes Dev. 9:2949-2963(1995).
 RN [5]
 RP SEQUENCE OF 570-639 FROM N.A.
 RC STRAIN-SNY243;
 RX MEDLINE-93087574; PubMed-1454852;
 RA Ramer S.W., Elledge S.J., Davis R.W.;
 RT "Dominant genetics using a yeast genomic library under the control of
 RT a strong inducible promoter.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:11589-11593(1992).
 CC -1- FUNCTION: GTPASE-ACTIVATING PROTEIN (GAP) FOR CDC42 AND/OR RHO1.
 CC NEGATIVE REGULATOR OF THE PHENOMENE-RESPONSE PATHWAY THROUGH THE
 CC STE20 PROTEIN KINASE; ACTS AT A STEP BETWEEN THE G-PROTEIN AND THE
 CC MAP KINASE MODULE. DOMINANT SUPPRESSOR OF BUD EMERGENCE DEFECT
 CC CAUSED BY DELETION OF IPL2/BEM2. INVOLVED IN THE CONTROL OF
 CC POLARIZED CELL GROWTH AND PROPER BUD SITE SELECTION.
 CC -1- SIMILARITY: CONTAINS 1 GAP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U07421; AAA16875.1; -;
 DR EMBL: X90518; CA62108.1; -;
 DR EMBL: X94335; CA64046.1; -;
 DR EMBL: Z73035; CA93926.1; -;
 DR EMBL: X90950; CA62445.1; -;
 DR EMBL: L02617; AAA35153.1; -;
 DR PIR: S48535; S48535;
 DR SGD: S0005653; RGA1;
 DR INTERPRO: IPR000198; -;
 DR INTERPRO: IPR001781; -;

DR PFAM: PF00412; LIM; 2.
 DR PFAM: PF00620; RhoGAP; 1.
 DR PROSITE: PS00478; LIM DOMAIN 1; 1.
 DR PROSITE: PS0023; LIM DOMAIN 2; 2.
 KW GTPase activation; Repeat; LIM motif; Metal-binding; Zinc;
 KW Phenomene response.
 FT DOMAIN 13 LIM.
 FT DOMAIN 70 LIM.
 FT DOMAIN 122 LIM.
 FT DOMAIN 805 977 GAP DOMAIN.
 FT MUTAGEN 40 40 C->S; BIPOLAR BUDDING.
 FT MUTAGEN 37 37 C->S; BIPOLAR BUDDING.
 FT MUTAGEN 98 98 C->S; BIPOLAR BUDDING.
 FT MUTAGEN 101 101 C->S; BIPOLAR BUDDING.
 FT VARIANT 866 866 V -> A.
 FT VARIANT 898 898 S -> R.
 FT VARIANT 926 926 S -> G.
 FT VARIANT 957 957 D -> E (IN REF. 4).
 FT CONFLICT 457 457 T -> P (IN REF. 4).
 FT CONFLICT 507 507
 SQ SEQUENCE 1007 AA; 112831 MW; C805411B57553791 CRC64;
 Query Match 7.9%; Score 87.5; DB 1; Length 1007;
 Best Local Similarity 25.0%; Pred. No. 16;
 Matches 45; Conservative 25; Mismatches 79; Indels 31; Gaps 9;
 QY 31 IPNLSVLYDSLPGRVNAESVERIKRRSSQ---EOTFOLKLMKHNRDQEWKKI.
 DB 804 IPMLISVCIDFESDEENMRS-EGTYRKSQSOLVTEIEIKOPSAAKVOQNT--TPNII 160
 QY 88 DIDLCSSVORHLGSHNLTTEOLLALMESLPCKKISPEIERTKTKSSSEQLKLT-- 143
 DB 861 EDDL-----NVTGVLKRYRLKLPPIPTFQIYEDMLNLSKMMEMELPYY 108
 QY 144 --LSLWRKND--ODITKGLMTALKHLKTSHP--KVTYSLKRTMPLH--STFM 195
 DB 909 GKLSTL-EAKNSDTYSSKSAKNLIEDLPREHYRLRVLSIEIKVTRYSHMNRATLYNL 967
 RESULT 8
 GINA_YEAST STANDARD: PRT; 1142 AA.
 AC 012263;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE GINA (EC 2.7.1.-).
 GN GINA OR YDR507C OR D9719.13.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99030835; PubMed-9813093;
 RA Longtine M.S., Fares H., Pringle J.R.;
 RT "Role of the yeast Gln4p protein kinase in septin assembly and
 RT relationship between septin assembly and septin function.";
 RL J. Cell Biol. 143:719-736(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Ber.
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin J.
 RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shoff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY PLAY A ROLE IN SEPTIN ASSEMBLY.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASE.
 CC NIMI SUBFAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL
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RA Guerout-Fleury A.M., Gonzy-Treboul G., Stragier P.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / JH642;
 RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
 RA Sato T., Takeuchi M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: U35252; AAA76726.1; -
 DR EMBL: D84432; BAA12566.1; -
 DR EMBL: 299116; CAB14368.1; -
 DR SUBMITTER: BG11414; spo111AC.
 KW Spotiation; Transmembrane.
 FT TRANSMEM 30 50
 FT CONFLICT 14 14 F -> S (IN REF. 2).
 SQ SEQUENCE 229 AA: 25549 MW: 110310C897BD8691 CRC64;

Query Match 7.6%; Score 84.5; DB 1; Length 229;
 Best Local Similarity 19.0%; Pred. No. 4.6;
 Matches 34; Conservative 44; Mismatches 48; Indels 53; Gaps 7;

OY 41 SLPGTKVNAESYERIKRRSS--SOEOTFOLKLMK-----HONRDEMYVK 84
 DB 51 SSKPEKNAKTTTAVSSQSSADSKETAIEYFKASKSDKPRDSIDDEYKEYNOLKELLET 110
 OY 85 II-----QDIDCESSV-ORHLGHSNLTTEQLALMESLPGRKISPEIEIETRTCK 135
 DB 111 IIGVDVSVVAVNDATSLKYERKNSKNKNTTEE-----TDKEGKRSVTDQ 157
 OY 136 SSKPOLKLLSLMRKRGDDT-----LKGIMYALKHLKTSHPRTVTHSLKTM 184
 DB 158 SSKPEIIVM-----TKNGDETPYVVOVKRPDIKRGVLVAQGVNVOIKOTIEAVTRVL 211

RESULT 11
 MYSA_MOUSE
 ID MYSA_MOUSE STANDARD; PRT: 1853 AA.
 AC 099104;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN VA) (MYOSIN 5A).
 GN MYOSA OR DILUTE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RA MEDLINE-91141583; PubMed-1996138;
 RA Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,
 RA Jenkins N.A.;
 RT "Novel myosin heavy chain encoded by murine dilute coat colour
 RT locus";
 RL Nature 349:709-712(1991).
 RN [2]
 RP REVISIONS.
 RA Mercer J.A., Seperack P.K., Strobel M.C., Copeland N.G.,
 RA Jenkins N.A.;
 RL Nature 352:547-547(1991).
 CC -I- FUNCTION: MAY BE INVOLVED IN MELANOSOME TRANSPORT OR
 CC ALTERNATIVELY, IT MAY BE REQUIRED FOR SOME POLARIZATION PROCESS
 CC INVOLVED IN DENDRITE FORMATION.

CC -I- SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE
 CC CALMODULIN OR MYOSIN LIGHT CHAINS.
 CC -I- SIMILARITY: BELONGS TO THE MYOSIN HEAVY CHAIN FAMILY. CLASS-
 CC MYOSIN SUBFAMILY.
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 DR EMBL: X57377; CAA40651.1; -
 DR PIR: A46761; A46761.
 DR HSSP: P08799; 1MND.
 DR MGD: MGI:105976; MYOSA.
 DR INTERPRO: IPR000048; -
 DR INTERPRO: IPR001609; -
 DR INTERPRO: IPR002710; -
 DR PFAM: PF01843; DIL; 1.
 DR PFAM: PF00612; IQ; 6.
 DR PFAM: PF00063; myosin_head; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 KW Myosin; Repeat; ATP-binding; calmodulin-binding; Actin-binding;
 KW Coiled coil; Phosphorylation.
 FT DOMAIN 1 765
 FT DOMAIN 766 913
 FT DOMAIN 914 1040
 FT DOMAIN 1041 1853
 FT DOMAIN 643 665
 FT DOMAIN 766 887
 FT REPEAT 766 790
 FT REPEAT 791 815
 FT REPEAT 816 837
 FT REPEAT 838 863
 FT REPEAT 864 888
 FT DOMAIN 773 787
 FT DOMAIN 796 810
 FT DOMAIN 821 835
 FT DOMAIN 844 862
 FT DOMAIN 869 884
 FT DOMAIN 892 906
 FT NP BIND 163 170
 FT MOD RES 1758 1758
 SQ SEQUENCE 1853 AA: 215594 MW: 503E93D48CA6B766 CRC64;

Query Match 7.5%; Score 83.5; DB 1; Length 1853;
 Best Local Similarity 24.5%; Pred. No. 69;
 Matches 27; Conservative 25; Mismatches 35; Indels 23;

OY 46 KYNAESYERIKRRHSSQ--QTFOLKLMKHONRDEMV-----KRILQ 99
 DB 909 KIEARSVERKKLHGMENKIMQLOKRVDEQNKDKYKLMKELTNLEGVYNSETEKLRN 1008
 OY 90 DICESSVORHLGHSNLTTEQLALMESLPGRKISPEIEIETRTCKSSQ 139
 DB 969 ERLQSEE-----EAVVATGRVLSLOEETAKLR--KDLQETRSKRSIEE 1011

RESULT 12
 SMC3_YEAST
 ID SMC3_YEAST STANDARD; PRT: 1230 AA.
 AC P47037;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CHROMOSOME SEGREGATION PROTEIN SMC3 (DA-BOX PROTEIN SMC3).
 GN SMC3 OR YJL074C OR J1049.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetata;
 OC Saccharomycetaceae; Saccharomyces.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W303;
 RX MEDLINE=9747309; PubMed=9335333;
 RA Michaelis C., Ciosk R., Nasmyth K.;
 RT "Cohesins: chromosomal proteins that prevent premature separation of
 RT sister chromatids."
 RL Cell 91:35-45(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rose M., Koeltter P., Entian K.D.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Sor F.J.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD BE
 CC PART OF A CHROMOSOME CONDENSATION MOTOR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
 CC FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y14278; CAAT4655.1; -
 DR EMBL: Z49349; CAAB9366.1; -
 DR EMBL: X88851; GAA61313.1; -
 DR SGI: S0003610; SMC3.
 KM Mitosis: ATP-binding; Coiled coil; Nuclear protein.
 FT NP_BIND 32 39 ATP (POTENTIAL).
 FT DOMAIN 172 482 COILED COIL (POTENTIAL).
 FT DOMAIN 685 1041 COILED COIL (POTENTIAL).
 FT SEQUENCE 1230 AA; 141336 MW; B152D88F780341F CRC64;
 SO SEQUENCE
 Query Match 7.5%; Score 83; DB 1; Length 1230;
 Best Local Similarity 21.6%; Pred. No. 46;
 Matches 43; Conservative 35; Mismatches 65; Indels 56; Gaps 11;
 QY 38 LVDSL--PGTVNAESV-----RIKRHSQEQTFOLKLMKHONROEMVKIITODIDL 91
 Db 445 LIDINGPDTGOLEDPESELIHLKOKLSESLDTRK--ELMRKQKLOTLETLSLVNQ 502
 QY 92 CESSVORHLGHSNLTTEBOLLALMESLPKGISPEIERT-----RKTCK----- 135
 Db 503 NORVNVETMSRS--LANCIINVKETTEKLTISPESVCTGLCELKLVNDKYTCAEVIGCN 560
 QY 136 -----SSQLKLKL--SLMRKING-----DOD-----TLKGLMYA--LKH 166
 Db 561 SLFHLVVDTEETATLIMELRYKMGKGRVTFIPLNRLSDSVKPPSNTTQIQFTPLKK 620
 QY 167 LK-TSHPKTYTHSLRKT 184
 Db 621 IKYPRFEKAVKHFVKGKI 639
 RESULT 13
 RBP2_PLAVB STANDARD: PRT: 1251 AA.
 AC 000799;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RETICULOCYTE BINDING PROTEIN 2 (FRAGMENT).
 GN RBP2.

OS Plasmodium vivax (strain Belem).
 NC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9231538; PubMed=1617731;
 RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
 RT "A reticulocyte-binding protein complex of Plasmodium vivax
 RT merozoites."
 RL Cell 69:1213-1226(1992).
 CC -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
 CC HUMAN RETICULOCYTE CELLS.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND (PROBABLE).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M88098; AAA29744.1; -
 KM Malaria; Receptor; Membrane.
 FT NON_TER 1
 FT NON_TER 1
 FT SEQUENCE 1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
 SO SEQUENCE
 Query Match 7.5%; Score 83; DB 1; Length 1251;
 Best Local Similarity 24.1%; Pred. No. 47;
 Matches 38; Conservative 32; Mismatches 50; Indels 38; Gaps 7;
 QY 39 VDSIPGTVNAESVRIKRHSQEQTFOLK--LMKHONROEMVKIITODIDLCS 1
 Db 954 IDSL-----MTADELLKKGKTCVSRKRLKIDVTVEISDTLIMT-----EKRY 401
 QY 97 QRHLGHSNLT--TEOLLALMESLPKGISPEIERTKTKSSQLKLKLS-----V 147
 Db 1002 KAVLAYIKKNVEDVQVLTLEHFNTRKQVSNHEPTNEDSKNSSEELTAVTDSKTI 1061
 QY 148 RIK-----NGQDT-----LKGLMYALKLTKTS 170
 Db 1062 KIKGVIIIVNENTEMNTSSAKIEIALYNELNKRKTS 1099
 RESULT 14
 PCNT_MOUSE STANDARD: PRT: 1920 AA.
 AC P48725;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE PERICENTRIN.
 DE PCNT.
 OS Mus musculus (Mouse).
 NC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94170365; PubMed=8124707;
 RA Doxsey S.J., Stein P., Evans L., Calarco P.D., Kirschner M.;
 RT "Pericentrin, a highly conserved centrosome protein involved in
 RT microtubule organization."
 RL Cell 76:639-650(1994).
 CC -1- FUNCTION: INTEGRAL COMPONENT OF THE FILAMENTOUS MATRIX OF THE
 CC CENTROSOME INVOLVED IN THE INITIAL ESTABLISHMENT OF ORGANIZING
 CC MICROTUBULE ARRAYS IN BOTH MITOSIS AND MEIOSIS.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN KIDNEY, THYMUS,
 CC LIVER, LOW LEVELS IN BRAIN, MUSCLE, LUNG AND HEART.
 CC -1- DOMAIN: COMPOSED OF A COILED-COIL CENTRAL REGION FLANKED BY
 CC HELICAL N- AND C-TERMINALS.
 CC -1- SIMILARITY: STRONG, TO HUMAN KENDRIN.

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CC or send an email to license@isb.ch).

DR EMBL: U05823; AAA1786.1; -
DR MGD: MGI:102722; PCNT.
KW Coiled coil; Microtubules.
FT DOMAIN 110 1600 COILED COIL (POTENTIAL).
FT DOMAIN 109 112 POLY-PRO.
FT DOMAIN 383 387 POLY-GLN.
FT SEQUENCE 1920 AA; 218337 MW; CFID0ADECB573309 CRC64;

Query Match 7.5%; Score 83; DB 1; Length 1920;
Best Local Similarity 22.5%; Pred. No. 79;
Matches 42; Conservative 35; Mismatches 86; Indels 24; Gaps 6;

QY 5 EATGCGCDVLTCEAFR-----FAVPTKIIPWLSVLSDEGKY-NAESVERIKR 57
DB 1002 ETSVCSEISSHWCESEFFIRPENTLDEQPIRRYOSLSSTAVALLEMAIDSSKOLEEARO 1061
QY 58 RISSQEOFTQLLKMKHONRODEWVKIIDDIDCESSVORHLGHSNLTTEQLLMEST 117
DB 1062 LHRCYERER-----KRNEMAMAMKOOLEERLEESNAADRLALE-LHRAKGLL 1112
QY 118 PCKKISPEIERFRTKSSSEQLLKLISLRKNGDODTLKGLMYALKHUKTSHPKTYT 177
DB 1113 EGFKEVKVDLQALGKKESEQOL-LTEL-----EDLRKQLEQAAARELLTLKEEKSVL 1164
QY 178 HSLRKT 184
DB 1165 WNKETL 1171

RESULT 15
ACVS-CEPAC STANDARD: PRT: 3712 AA.
ID ACVS-CEPAC
AC P25464:
RT 01-MAY-1992 (Rel. 22, Created)
RT 01-MAY-1992 (Rel. 22, Last sequence update)
RT 15-JUL-1998 (Rel. 36, Last annotation update)
DE DELTA-(L-ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE SYNTHETASE
DE (EC 6.-.-.-) (ACV SYNTHETASE) (ACVS).
GN PCBAB.
OS Cephalosporium acremonium (Acremonium chrysogenum).
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Acremonium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91177827; PubMed-1706706;
RA Gutierrez S., Diaz B., Montenegro E., Martin J.F.;
RT "Characterization of the Cephalosporium acremonium pcbaB gene
RT encoding alpha-aminoadipyl-cysteine-lyl-valine synthetase, a large
RT multidomain peptide synthetase: linkage to the pcbaC gene as a cluster
RT of early cephalosporin biosynthetic genes and evidence of multiple
RT functional domains".
RL J. Bacteriol. 173:2354-2365(1991).
RN [2]
RP PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-ATCC 11550;
RX MEDLINE-91168300; PubMed-2076552;
RA Hoskins J.A., O'Callaghan N., Queener S.W., Cantwell C.A., Wood J.S.,
RA Chen V.J., Skatrud P.L.;
RT "Gene disruption of the pcbaB gene encoding ACV synthetase in
RT Cephalosporium acremonium".
RL Curr. Genet. 18:523-530(1990).
CC -I- FUNCTION: EACH OF THE CONSTITUENT AMINO ACIDS OF THE TRIPEPTIDE
CC ACV ARE ACTIVATED AS AMINOACYL-ADENYLATES WITH PEPTIDE BONDS
CC FORMED THROUGH THE PARTICIPATION OF AMINO ACID THIOLESTER
CC INTERMEDIATES.

CC -I- COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTHETHEINES
CC (POTENTIAL).
CC -I- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF PENICILLIN AND
CC CEPHALOSPORIN.
CC -I- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR PIR: A38531; YGCEVC.
DR HSRP: P14687; 1AMU.
DR INTERPRO: IPR000255; -
DR INTERPRO: IPR000873; -
DR INTERPRO: IPR001031; -
DR INTERPRO: IPR001242; -
DR PFAM: PF00501; AMP-binding: 3.
DR PFAM: PF00668; DUF4: 3.
DR PFAM: PF00975; Thioesterase: 1.
DR PFAM: PF00975; Thioesterase: 1.
DR PFAM: PF00550; PP-binding: 3.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; 2.
DR PROSITE: PS00455; AMP BINDING; 3.
DR PROSITE: PS00755; ACP-DOMAIN; 3.
KW Liase; Antibiotic biosynthesis; Multifunctional enzyme;
KW Repeat; Phosphopantetheine.
FT REPEAT 234 1062 DOMAIN 1 (ADIPATE-ACTIVATING).
FT REPEAT 1335 2162 DOMAIN 2 (CYSTEINE-ACTIVATING).
FT REPEAT 2409 3387 DOMAIN 3 (VALINE-ACTIVATING).
FT DOMAIN 795 864 ACYL CARRIER (ACP).
FT DOMAIN 1880 1953 ACYL CARRIER (ACP).
FT DOMAIN 2960 3027 ACYL CARRIER (ACP).
FT BINDING 827 827 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT BINDING 1916 1916 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT BINDING 2990 2990 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT ACT SITE 3568 3568 THIOESTERASE (BY SIMILARITY).
SQ SEQUENCE 3712 AA; 414767 MW; 4EB3C1EB5BEEF9B7 CRC64;

Query Match 7.5%; Score 83; DB 1; Length 3712;
Best Local Similarity 23.5%; Pred. No. 1,8e+02;
Matches 46; Conservative 35; Mismatches 85; Indels 30; Gaps 10;

QY 14 VTLCEAFRRFVPTKI-----IPWLSVLD--SLPRTKNAESVEIKRRHSQEQ 6
DB 739 LSELEKLLPRYWPVPRLOLAQIPNIGKADLRALPAVEVAVAPTRHODERGNQLLS 97
QY 67 QLLKMKHONRODEWVKIIDDIDCESSVORHLGHSNLTTEQLLMESTLPGKKISPEI 126
DB 798 DLAIWGN-----ILSPADIDG-SESNFRLGSH-IACIOLARQOLGOSITIT 19
QY 127 IERTPKTKSSSEQLLKLISLRKNGDODTLKGLMYALKHUKTSHPKTYT----- 176
DB 850 VQGT-KTLRAMALLIS-EKTKASNGTNGVTGTAHVGHANGHVSIVASSLQGGI 107
QY 177 THSLKRTMRFLHSFTM 192
DB 908 YHSLKNEIS--EAYTM 921

Search completed: January 27, 2001, 11:24:56
Job time: 138 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:37 ; Search time 25.38 seconds

(without alignments)
577.878 Million cell updates/sec

Title: US-09-389-545-2_COPY_186_401
Perfect score: 1113
Sequence: 1 SGNREATORCGIDVTLCBEA.....OKLFLEMIGNQGVSKISCL 216
Working table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR-66:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	9.0	1574	1 A38454	myosin MYO2 - yeast
2	95.5	8.6	697	2 T37827	hypothetical prote
3	95	8.5	203	2 T14848	MADS-box protein d
4	95	8.5	486	2 T21481	hypothetical prote
5	92	8.3	1309	2 T39379	sexual differentia
6	91.5	8.2	901	2 JC7111	tetratricopeptide
7	91.5	8.2	1208	2 T39068	coiled coil protei
8	91	8.2	1364	2 T14900	condensin XCAP-D2
9	90.5	8.1	463	2 T32289	hypothetical prote
10	90	8.1	463	2 C71665	chromosomal replic
11	88.5	8.0	710	2 T22360	hypothetical prote
12	88.5	8.0	1388	2 T30335	KIP2 protein - Afr
13	88	7.9	361	2 T50691	basic-leucine zipp
14	88	7.9	523	2 T19684	hypothetical prote
15	88	7.9	1017	2 PC4035	cell-cycle-depende
16	88	7.9	1225	2 A56514	chromokinesin - ch
17	87.5	7.9	1007	2 S48535	rho-type GTPase-ac
18	87	7.8	823	2 D70386	probable polyketid
19	87	7.8	1235	2 B72029	helicase, Suf2/Rad
20	87	7.8	4151	2 T13734	groovin gene prote
21	86.5	7.8	1142	2 S59359	GIN4 protein - yea
22	86	7.7	1442	2 C82898	DNA polymerase III
23	86	7.7	1837	2 T41023	probable nuclear p
24	86	7.7	2677	2 A38194	desmoplakin I - hu
25	84.5	7.6	229	2 B69712	mutants block spor
26	84.5	7.6	764	2 T51302	myosin heavy chain
27	84.5	7.6	812	2 A53016	myosin heavy chain
28	84	7.5	451	2 T21036	hypothetical prote
29	84	7.5	1226	2 T51617	kinesin-like prote

ALIGNMENTS

RESULT 1

A38454 myosin MYO2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O6167; protein YOR326w
C:Contents: myosin ATPase (EC 3.6.1.32)
C:Species: Saccharomyces cerevisiae
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-
C:Accession: A38454; S58339; S62058; S67232; S67233; S71966; S72005
R:Johnston, G.C.; Prendergast, J.A.; Singer, R.A.
J. Cell Biol. 113, 539-551, 1991
A:Title: The Saccharomyces cerevisiae MYO2 gene encodes an essential protein for vecto
A:Reference number: A38454; MIMD:91201404
A:Accession: A38454
A:Molecule type: DNA
A:Residues: 1-1574 <JOH>
A:Cross-references: EMBL:355332; NID:q172021; PIDD:AAA34810.1; PID:q17-
R:Pearson, B.M.; Hernandez, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
submitted to the EMBL data library, August 1995
A:Reference number: S58339
A:Accession: S58339
A:Molecule type: DNA
A:Residues: 1-748 <PEA>
A:Cross-references: EMBL:X00565; NID:q940836; PIDD:CAA62184.1; PID:q94-
R:Parle, A.G.; Hand, N.J.; Goulding, S.G.; Wolfe, K.H.
Submitted to the EMBL data library, June 1995
A:Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sa
A:Reference number: S62058
A:Accession: S62058
A:Molecule type: DNA
A:Residues: 677-1574 <PAR>
A:Cross-references: EMBL:249821; NID:q1163062; PIDD:CAA89973.1; PID:q11-
R:Pearson, B.M.; Hernandez, Y.; Kalogeropoulos, A.; Schweizer, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67213
A:Accession: S67213
A:Molecule type: DNA
A:Residues: 1-748 <PEW>
A:Cross-references: EMBL:275234; GSPDB:GN00015; MIPS:YOR326w
A:Experimental source: strain S288C
R:Goulding, S.E.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67233
A:Accession: S67233
A:Molecule type: DNA
A:Residues: 677-1574 <GOU>
A:Cross-references: EMBL:275234; GSPDB:GN00015; MIPS:YOR326w
A:Experimental source: strain S288C
R:Parle-McDermott, A.G.; Hand, N.J.; Goulding, S.E.; Wolfe, K.H.
Yeast 12, 999-1004, 1996
A:Title: Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces c
A:Reference number: S71966; MIMD:97051586
A:Accession: S71966

myosin heavy chain
hypothetical prote
hypothetical prote
SMC1 protein homol
reticulocyte-Dnbl
pericenturin - mous
alpha-aminoadipyl-
hypothetical prote
hypothetical prote
viral integrase
conserved in yeast
probable protein-cane
transcriptase term
transcription term
hypothetical prote
ribosomal protein

34 WL---SYLVDSLBPTKVNAESVERIKRHRHSQEQTFQLKLKHKHQRDQEMVKKTC

Db 967 WLEBERSILIDELBSYRNOFNON-----NLVODKNELERLEKELOEL 1011
 Oy 90 DLCSNV--QRHGHSLNLTTE---QLALMESLPCKRISPEE-----LERTKTKCKSSQOL 140
 Db 1012 EYNNHMKQALMTNSVTDSQMLKTLREALOSKTNNDHSLTLERKREKYS----- 1067
 Oy 141 LKLISLW-----RIKNGDQDT-----LKLIMYALKHKTSHFPPTVTHSLRKT 183
 Db 1068 --LDDYQNLARKNLQSNPNQSGQSESEIKGLSKLRYLQSKCRRE---HSLULD 1122
 Oy 184 MRLHSF-----TKRLYOKLFLEKIGNOVOSKIS 214
 Db 1123 LAFSKFIMQLTGTECNKINLRML---OKIGIS 1154

RESULT 8
 T14900
 condensin XCAP-D2 chain - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
 C:Accession: T14900
 R:Kimura, K.; Hirano, M.; Kobayashi, R.; Hirano, T.
 Science 282, 487-490, 1998
 A:Title: Phosphorylation and activation of 13S condensin by cdc2 in vitro.
 A:Reference number: Z18257; MUID:98447791
 A:Accession: T14900
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1364 <KIM>
 A:Cross-references: EMBL:AF067969; NID:93764086; PID:93764087; PIDN:AAC64359.1

Query Match 8.2%; Score 91; DB 2; Length 1364;
 Best Local Similarity 20.8%; Pred. No. 34;
 Matches 54; Conservative 34; Mismatches 68; Indels 104; Gaps 10;

Oy 4 REATQKCIDVTLCBEAFPRFA-----VPRKIIPNLSVLVDLSLPGTK----- 46
 Db 276 REIGCKCQSDLSRESSGKFAFETLELAEERIPALMPS--ISVLIDYDGENYMMRNSVL 334
 Oy 47 -VNAESVRI-----KRRHSOQOTFOLKIMKHQ----- 75
 Db 335 TVMGEMVVRVLVSGDQLEAEKSSRQPLDTLOEHLHDVNTVRSVCVIOIYNRIVOEKALP 394
 Oy 76 -NRDQEMVKIIT---ODIDLCSSVQ---RHLSHSLNT-----TEQLL 111
 Db 395 LSRFSVVTIVVGRFLDQSVNCKNAIQLLASFLANNPFTCKLSVDLKVLEKETKIKL 454
 Oy 112 ALMESLPCKR---ISPE-----ELERTKTKCKSSQOL 140
 Db 455 EMREKYQCPKPVVVISPEEWEAMLPEVLEAFKILQESKEEDEDIETEIESSQHLRQOI 514
 Oy 141 LKLISLWIKNGDDDTLKL 160
 Db 515 LILKRTSYKNSIRLTOKGI 534

RESULT 9
 T32289
 hypothetical protein F4262.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32289
 R:Schaeft, P.; Maggi, L.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of C. elegans cosmid F4262.
 A:Reference number: Z21146
 A:Accession: T32289
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-833 <SCH>
 A:Cross-references: EMBL:AF024499; PIDN:AAV70358.1; GSPDB:GN00020; CESP:F4262.6
 A:Experimental source: strain Bristol N2; clone F4262

C:Genetics:
 A:Gene: CESP:F4262.6
 A:Map position: 2
 A:Introns: 317/1; 335/1; 362/3; 781/1

Query Match 8.1%; Score 90.5; DB 2; Length 833;
 Best Local Similarity 29.7%; Pred. No. 21;
 Matches 33; Conservative 17; Mismatches 42; Indels 19; Gaps 4;

Oy 54 RIKRRHSQEQTFOLKLV-KHQRDQEMVKIITQDIDLCSSVQRL----- 100
 Db 679 RKKLRMSKRQONELLOALWKEKNTENTHAETNOEKRLNNVOLEQMMKIOEPA 738
 Oy 101 -GHSNLTTEQL-LALMESLPCKRISPEEIE---RTKTKCKSSQOLKILS 145
 Db 739 AADSKNLKEQWVLEMDKIDDAQETRIKELEVEYKSKNKKGEQLDLRS 789

RESULT 10
 C71665
 chromosomal replication initiator protein dnaa (dnaa) Rp601 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 20-Jun 2000
 C:Accession: C71665
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Poulsen, T.; Alsmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria
 A:Reference number: A71630; MUID:99039499
 A:Accession: C71665
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-463 <AND>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:93861033; PIDN:CAV1 1.1; PID:9386
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: dnaa; Rp601
 C:Superfamily: replication initiation protein dnaa

Query Match 8.1%; Score 90; DB 2; Length 463;
 Best Local Similarity 23.8%; Pred. No. 12;
 Matches 49; Conservative 36; Mismatches 61; Indels 60; Gaps 12;

Oy 10 CGIDVTLCBEAFPRFAFPIIIPNLSVLV--DSLPTKYNAESVERIKRR----- 148
 Db 237 CGKQSTQ-EEFFHTF---NLLIDNNRQAVISCDSPSDDNIE--DRIKRRLQMGVALAV 290
 Oy 59 HSSQEQTFOLKIMKHQRDQEM-----VKIITQDIDLCSSVQRLHSHSLNT 106
 Db 291 HST---TYE-LRLGILTSKIEQMNVKIPKDVINFLASKIVSNVRELEGALNKVIAHSNFT 146
 Oy 107 TEQLALMESLPCKRISPEEIER-TRTKCKSSQOL-----KLISLWIKNGDDDTL 158
 Db 347 L-----KATILEMTQNLRLDLRSNERIIVEDIQKVASRYNIKUSD----- 189
 Oy 159 GLMYALKHKTSHFPKTVTTHSLRKT 184
 Db 390 --WYSSRLREVARPROIAMYLSKTL 413

RESULT 11
 T22360
 hypothetical protein F4764.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22360
 R:White, S.
 submitted to the EMBL Data Library, September 1997
 A:Reference number: Z19553
 A:Accession: T22360
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

00 100 FUNDAMENTAL 199

```

      .      | :: | | | : |
Db 414  ALNAGPMYNLQENL 427

```

RESULT 15

PC4035

cell-cycle-dependent 350K nuclear protein - human (fragment)

C;Species: Homo sapiens (man)

C:\Accession\PCA035
C:\Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C;Accession: PC4035
P.T: 0 : K Y : K

R; Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshl, H.C.
Biochem Biophys Res Commun 212:220-228, 1995

A·Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for

A:Reference number: PC4035; MUID:95336446

A: Accession: PC4035

```

A:Molecule type: DN

```

```

A;Residues: 1-1017 <

```

A; Cross-references: GB:U

A;Note: repeat 15-160 and 200-340

C;Comment: This protein contains

C; Keywords: nucleoprotein; phosphoprotein

F;465/Binding site: phosphate (Thr) (cova

F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status

F;908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pr

1

Query match	Score	DB 2;	Length
7.98;	88;	DB 2;	Length 1017;

Best Local Similarity 23.48; Pred. No. 41;

Matches	40;	Conservative	34;	Mismatches	55;	Indels	42;	Gaps	9;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

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QY      50 ESVERIKRRHSSQEQTFOLL-----KLWKHQNRD-----QEMVKKI-----IQD 88

```

db 425 EISRLKŃIQĐQĖLVSLSQVEGEHQLWKEŃNLLELRLNLTVELLEQKIQVLQSKNASLQĐ 484

89 -IDCESSVQRHLGHSNLTTEQLLALMESLPGKKISPEIER-----TRKTCSSQLLK 142

Db 485 TLEVQSSYKNLENELETKMDKMSFEVEKVNKMTAKETELQREHHEMAQKTAELQEE - - 542

QY 143 LLSLWRIKNGDQDTLKG-LMYALKHLKTSHER-KTVT---HSLRKTMRFLH 188

Db 543 -----SGEKNRLAGELQLLLEIKSSKDQLKELTLENSELKKS LDCMH 585

Search completed: January 27, 2001, 11:23:12
Job time: 35 sec

Job time: 35 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2001, 11:22:38 ; Search time 32.57 seconds
(without alignments)
226.769 Million cell updates/sec

Title: US-09-389-545-2_COPY_186_401
Perfect score: 1113
Sequence: 1 SGNEAQQKGGIDVTLCEFA.....OKLFLEMIGNQVSKISCL 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_36:*

- 1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT:*
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- 9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	401	18 W83344	Mouse osteoprotegerin
2	1073	96.4	208	20 W89231	Mouse osteoprotegerin
3	1069	96.0	401	18 W83343	Rat osteoprotegerin
4	1029	92.5	208	20 W89230	Rat osteoprotegerin
5	977	87.8	360	17 R99936	Mutated OCIF, OCIF
6	977	87.8	380	17 R99924	Mature osteoclasto
7	977	87.8	391	19 W53238	Human OCIF genome
8	977	87.8	401	17 R99925	Pull length osteoc
9	977	87.8	401	19 W53239	Human OCIF genome
10	977	87.8	401	20 Y05742	Tumour necrosis fa
11	977	87.8	401	20 W95030	Tumour necrosis fa
12	977	87.8	401	20 W83926	Human FTHMA-070 pr

13	972	87.3	359	17 R99937	Mutated OCIF, OCIF
14	972	87.3	401	19 W57635	FTH receptor, prote
15	969	87.1	401	18 W83345	Human osteoprotege
16	969	87.1	401	21 Y43400	Osteoprotegerin pro
17	967	86.9	359	17 R99939	Mutated OCIF, OCIF
18	967	86.9	401	17 R99932	Mutated OCIF, OCIF
19	967	86.9	401	17 R99935	Mutated OCIF, OCIF
20	967	86.9	401	17 R99931	Mutated OCIF, OCIF
21	964	86.6	359	17 R99942	Mutated OCIF, OCIF
22	964	86.6	401	17 R99933	Mutated OCIF, OCIF
23	962	86.4	401	17 R99934	Mutated OCIF, OCIF
24	960	85.3	360	17 R99938	Mutated OCIF, OCIF
25	949	85.3	420	20 W89224	Tumour necrosis fa
26	946	85.0	208	20 W89232	Human osteoprotege
27	932	83.7	417	20 W89226	Tumour necrosis fa
28	931	83.6	393	17 R99948	Mutated OCIF, OCIF
29	929	83.5	395	19 W57636	Modified FTH recep
30	833	74.8	397	20 W89227	Tumour necrosis fa
31	779.5	70.0	390	17 R99357	Human tumour necr
32	749	67.3	351	17 R99943	Mutated OCIF, OCIF
33	695.5	62.5	366	20 W89228	Tumour necrosis fa
34	621	55.8	327	17 R99941	Mutated OCIF, OCIF
35	592	53.2	321	17 R99949	Mutated OCIF, OCIF
36	569.5	51.2	326	17 R99940	Mutated OCIF, OCIF
37	558.5	50.2	349	20 W89928	Human FTHMA-070 pr
38	446.5	40.1	311	20 W89229	Tumour necrosis fa
39	416	37.4	272	17 R99944	Mutated OCIF, OCIF
40	100	9.0	590	21 Y83089	F-box protein PBP
41	91.5	8.2	228	20 Y25896	Human secreted pro
42	89	8.0	3248	17 R99795	Kineochore protei
43	88	7.9	2482	16 W28286	Human mitoch. HC
44	88	7.9	2482	16 W23996	Human mitoch. HC
45	86	7.7	1752	20 Y07031	Breast cancer asso

ALIGNMENTS

RESULT 1	
ID W83344	standard; Protein: 401 AA.
XX W83344;	
AC	
XX	
DT	20-APR-1998 (first entry)
XX	
XX	
DE	Mouse osteoprotegerin.
XX	
KW	Osteoprotegerin; antibody; diagnosis; affinity purification;
KW	recombinant production; transgenic animal; treatment; prevention.
KW	antislense oligonucleotide; probe; detection; screening; mouse;
KW	bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW	hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW	osteolytic metastasis; periodontal bone loss; bone necrosis;
KW	osteopentia; murine.
OS	Mus sp.
XX	
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS 90..1295
FT	/*tag= a
FT	/product= osteoprotegerin
XX	
XX	DE19654610-A1.
XX	
XX	26-JUN-1997.
XX	
XX	20-DEC-1996; 96DE-1054610.
XX	
XX	03-SEP-1996; 96US-0706945.
PR	22-DEC-1995; 95US-0577788.
XX	
XX	(AMGE-) AMGEN INC.

XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
XX WPI: 1997-334271/31.
DR N-PSDB; T96062.
XX

PT Nucleic acid encoding osteoprotegerin - useful for treatment of
PT diseases involving excessive bone loss, e.g. osteoporosis
XX
PS Claim 23; Pages 106-107; 182pp; German.

CC The present sequence is mouse osteoprotegerin (OPG). Anti-OPG
CC antibodies can be used in OPG diagnostic assays, and as affinity
CC purification materials. The OPG cDNA can be used to express
CC recombinant OPG and to generate transgenic animals. It can also
CC be used to regulate the level of OPG in mammals, specifically to
CC increase OPG levels, however the use of antisense sequences is
CC also contemplated. Fragments of the cDNA can be used as probes to
CC detect OPG expressing cells and tissue, and to screen cDNA
CC libraries for related sequences. OPG can be used to treat or
CC prevent bone diseases, specifically excessive bone loss, e.g.
CC osteoporosis, Paget's disease, hypercalcaemia,
CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC osteolytic metastases, periodontal bone loss, bone necrosis and
CC osteopaenia.

XX Sequence 401 AA;

Query Match 100.0%; Score 1113; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 6.6e-107;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGNRATQKCGIDVTLCEAFRFAVPTKIIPNMLSVLVDSPGKVAESVERIKRRHS 60
DB 186 sgnraatqkcgidvltlceafrrfapvkilpnwlsvldspgkvaesverikrrhs 245
OY 61 SOEQTFOLKLMKHONRDOEMVKRIIDIDLCSSVORHLSNLTTEQLALMESLPK 120
DB 246 sqeqtfqlklwkhqndqemvkkilqdidlcassvgrhlsnltteqlalmeslpk 305
OY 121 KISPEIRTRKTKCKSSQQLKLKLSMRKNGDDDTLGLMVALKHLKTSHPKTVHSL 180
DB 306 kispeltrtrtkckssqqlklklsmrkngdddtlglmvalkhlktsfptvthsl 365
OY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216
DB 366 rktmrflhsftmyrlyqkfllemignqvsvkiscsl 401

RESULT 2
W89231
W89231 standard; Protein; 208 AA.

XX W89231;

XX 04-MAR-1999 (first entry)

XX Mouse osteoprotegerin dimerisation domain.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.

XX Mus sp.

XX W09849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98MO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI: 1999-034661/03.

PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders

XX Disclosure; Fig 1; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents mouse OPG dimerisation domain.

XX Sequence 208 AA;

Query Match 96.4%; Score 1073; DB 20; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.6e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 KCGIDVTLCEAFRFAVPTKIIPNMLSVLVDSPGKVAESVERIKRRHSOQTFOL 68
DB 1 kcgidvltlceafrrfapvkilpnwlsvldspgkvaesverikrrhsqeqtfql 60
OY 69 LKMKHONRDOEMVKRIIDIDLCSSVORHLSNLTTEQLALMESLPKTRKSPK 128
DB 61 lkmkhondemvkkilqdidlcassvgrhlsnltteqlalmeslpktrkspek 120
OY 129 RTRKTKSSQQLKLKLSMRKNGDDDTLGLMVALKHLKTSHPKTVHSLRKTMRFL 188
DB 121 rtrtkckssqqlklklsmrkngdddtlglmvalkhlktsfptvthslrktmrfl 180
OY 189 SFTMYRLYOKLFLEMIGNOVSVKISCL 216
DB 181 sftmyrlyqkfllemignqvsvkiscsl 208

RESULT 3
W38343
W38343 standard; Protein; 401 AA.

XX W38343;

XX 20-APR-1998 (first entry)

XX Rat osteoprotegerin.

XX

KW Rat; osteoprotegerin; antibody; diagnosis; affinity purification;
KW recombinant production; transgenic animal; treatment; prevention;
KW antisense oligonucleotide; probe; detection; screening;
KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; bone necrosis;
KW osteopaenia.

XX

XX Rattus sp.

XX

PN DE19654610-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96DE-1054610.
 XX
 PR 03-SEP-1996; 96US-0706945.
 PR 22-DEC-1995; 95US-0577788.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
 DR WPI: 1997-334271/31.
 DR N-PSDB; T96061.
 PT Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis
 PS
 PS Claim 23; Pages 102-104; 182pp; German.
 CC The present sequence is rat osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express
 CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopentia.
 CC
 CC Sequence 401 AA;
 SQ
 Query Match 96.0%; Score 1069; DB 18; Length 401;
 Best Local Similarity 95.4%; Pred. No. 2.3e-102;
 Matches 206; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 PY 1 SGNREATORCGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHS 60
 DB 186 SGNREATORCGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHS 245
 QY 61 SGNREATORCGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHS 120
 DB 246 SGNREATORCGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHS 305
 QY 121 KTSPEIERTRKTCSSSEQLKLSLWRKINGDODTLKGLMALKHLKTSHPKTVTHSL 180
 DB 306 KTSPEIERTRKTCSSSEQLKLSLWRKINGDODTLKGLMALKHLKTSHPKTVTHSL 365
 QY 181 RKTMRPLSHFTMYRLYOKLFLEMIGNOVSVKISCL 216
 DB 366 RKTMRPLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 RESULT 4
 ID W89230 standard; Protein: 208 AA.
 AC W89230;
 DT 04-MAR-1999 (first entry)
 DE Rat osteoprotegerin dimerisation domain.
 XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
 KM OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis.

XX
 OS Rattus sp.
 XX
 PN WO9849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 29-APR-1998; 98WO-US08631.
 XX
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Wooden S;
 DR WPI: 1999-034661/03.
 PT New chimeric osteoprotegerin polypeptides - contain the
 PT osteoprotegerin dimerisation domain and a heterologous sequence.
 PT useful to treat TNF and TNFR-mediated disorders
 PS
 PS Disclosure; Fig 1; 92pp; English.
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The A1
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and
 CC ligands. The present sequence represents rat OPG dimerisation domain.
 CC
 CC Sequence 208 AA;
 SQ
 Query Match 92.5%; Score 1029; DB 20; Length 208;
 Best Local Similarity 95.7%; Pred. No. 1.3e-98;
 Matches 198; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 10 CGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHSOETPK 60
 DB 2 CGIDVTLCEAFPRFAVPTKIIPNMLSVLVDSPGTFVNAESVERIKRRHSOETPK 120
 QY 70 KLMKHNDRDQEMVKKIIDDIDLCSSVORHLGHSNLTTEQLALMESLPGKISPEET 120
 DB 62 KLMKHNDRDQEMVKKIIDDIDLCSSVORHLGHSNLTTEQLALMESLPGKISPEET 240
 QY 130 TRKTKSSSEQLKLSLWRKINGDODTLKGLMALKHLKTSHPKTVTHSLRKTMRPL 180
 DB 122 TRKTKSSSEQLKLSLWRKINGDODTLKGLMALKHLKTSHPKTVTHSLRKTMRPL 360
 QY 190 FTMYRLYOKLFLEMIGNOVSVKISCL 216
 DB 182 FTMYRLYOKLFLEMIGNOVSVKISCL 208
 RESULT 5
 ID R99936 standard; Protein: 360 AA.
 AC R99936;
 DT 23-APR-1997 (first entry)
 DE Mutated OCIF, OCIF-DCRI.

[illegible]

ID	R99924	standard; Protein; 380 AA.
XX		
AC	R99924;	
XX		
DT	22-APR-1997	(first entry)
XX		
DE	Mature osteoclastogenesis inhibitory factor.	
XX		
KM	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorp	tion;
XX	osteoporosis.	
OS	Homo sapiens.	
XX		
PN	W09626217-A1.	
XX		
PD	29-AUG-1996.	
XX		
PF	20-FEB-1996;	96WO-JP00374.
XX		
PR	21-JUL-1995;	95JP-0207508.
XX		
PR	20-FEB-1995;	95JP-0054977.
XX		
PA	(SNOW) SNOW BRAND MILK PROD CO LTD.	
PI	Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;	
PI	Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;	
XX		
DR	WPI; 1996-402320/40.	
XX	N-PSDB; T36685.	
PT	DNA encoding osteoclastogenesis inhibitory factor protein - used	for bone resorption control, esp. treatment of osteoporosis
XX		
PS	Claim 6; Page 62-64; 183pp; Japanese.	
XX		
CC	This sequence represents the mature osteoclastogenesis inhibitory	
CC	factor (OCIF) of the invention. The OCIF has a molecular weight by	
CC	SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-	
CC	reducing conditions. The protein is adsorbed onto cation-exchangers	
CC	or heparin and its activity is lowered after 10 mins at 70 deg.C or	
CC	30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is	
CC	useful in the control of bone resorption and therefore in the	
CC	treatment and prevention of disorders of bone resorption, e.g.	
CC	osteoporosis.	
SQ	Sequence	380 AA;
Query Match	87.8%;	Score 977; DB 17; Length 380;
Best Local Similarity	85.2%;	Pre. No. 6.9e-93;
Matches 184; Conservative 19; Mismatched 13; Indels 0; Gaps 0;		
QY	1	SGNRATQKCGIDVYLCEAFRFAVPRKIIIPNMLSYVYDLSIPGKVAESVERIKRHS 60
DB	165	sgnsstctkcgdvylceaafrfaavprkfpnwslsvyvdnlpqknaesverikrghs 224
QY	61	SOEQTFQQLKLMKHONRQENWVKIIOIDIDLCSSVQRHLGHSNLTTEQLALMESLPGR 120
DB	225	sqeqtfqllklwkhqkqgdvkkkigdidlcensvqrhlgshantfeqlslmeslpgr 284
QY	121	KISPEIERTKTKCSSQQLKLSLRINKGDDDTLGLMYALKHLKTSHPPTVTHS 180
DB	285	kvsgeadiektklckpsdqllkllslwrlkngddqtlkglmaalkshsktyhfpkvtqsl 244
QY	181	RKTMFLHSFTMYRKYOKLFLEMTGNQVSKISL 216
DB	345	kktirflhsftmyklygkflflemignqgsvskisl 380
RESULT	7	
W53238		
ID	W53238	standard; Protein; 391 AA.
XX		

AC		W53238:	
XX		15-JUL-1998	(first entry)
DE		Human OCIF genome DNA-2 protein.	
XX		Human; OCIF: genome; osteoclast; antipyretic; osteoporosis;	
KV		rheumatism; multiple sclerosis.	
XX		Homo sapiens.	
OS		MO9807840-A1.	
PN		26-FEB-1998.	
PD		19-AUG-1997;	97WO-JP02859.
XX		19-AUG-1996;	96JP-0235928.
PR		(SNOW) SNOW BRAND MILK PROD CO LTD.	
PA		Morinaga T, Nakagawa N, Yasuda H;	
PI		WPI: 1998-169150/15.	
DR		N-PSDB: V20767.	
PT		Inhibition of osteoclast formation and/or antipyretic activity -	
PT		useful for, e.g. treating osteoporosis, rheumatism and multiple	
PT		sclerosis	
XX		Disclosure: Page 16-26; 36pp; English.	
PS		The present sequence represents human OCIF genome DNA protein	
CC		which is shown in the present invention. The present invention	
CC		describes: (i) a method of inhibiting the formation of osteoclasts	
CC		and/or antipyretic proteins, which have the following characteristics:	
CC		(i) MW determined by SDS-PAGE of approximately 60 kDa under reducing	
CC		conditions, and 60 kDa and 120 kDa under non-reducing conditions; (ii)	
CC		401 aa sequence (iii) (see W53239); (iii) affinity to cation exchangers	
CC		and heparin; (iv) its osteoclast formation inhibiting activity reduced	
CC		by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius	
CC		for 30 minutes, and (v) its antipyretic activity reduced by heating at	
CC		90 degrees Celsius for 10 minutes, and (2) a method for preparing the	
CC		above proteins. The proteins are useful for, e.g. treatment and	
CC		prevention of osteoporosis, rheumatism or multiple sclerosis, and also	
CC		as antigens for immunological diagnosis of these diseases and disorders.	
XX		Sequence 391 AA:	
SO			
	Query Match	87.8%; Score 977; DB 19; Length 391;	
	Best Local Similarity	85.2%; Pred. No. 7.2e-93;	
	Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0		
OY	1	SGNRKATOKCGIDVTLCBAFFRFPVKIIPNMLSVLVDLSLPGRKVNAESVERIKRRHS	60
PB	176	sgnsestlqkgidvlceaeaffrfaupkfpbnwslvldanpgtckvnaesverikrrhs	235
OY	61	SQEOFFOLLIKLMMKHNNROEMWKRIIODDICESSVORHIGSNTTTEDLALMESTLPCK	120
PB	236	sgeqdfqlklmkhnpqgdvllkdiddlcemsvgrilghnantlfedrlmeslpck	295
OY	121	KISPEIRTRTKTCSSBDQLKLTLMLRKNDODOTLKGLMALHLKTSHPKTYTHSL	180
PB	296	kvgaediektlkackpsdglklkslwrlngdgdtllgmalhlkskyhpkctvtgs1	355
OY	181	RKTARFLHSFTWRLYOKLFLEMIGNOVOSVAKISCL	216
PB	356	kttirflnsftmykiyqkiflemignqvsvskisc1	391

ID	R99925 standard; Protein; 401 AA.
XX	
AC	R99925;
XX	
DT	22-APR-1997 (first entry)
XX	
DE	Full length osteoclastogenesis inhibitory factor.
XX	
KW	Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resor-
RW	osteoporosis.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	/note= "Signal peptide"
FT	Protein
FT	/note= "Mature OCIF, claim 6"
XX	
PV	M09626217-AI.
XX	
PD	29-AUG-1996.
XX	
PF	20-FEB-1996; 96MO-JP00374.
XX	
PR	21-JUL-1995; 95JP-0207508.
PR	20-FEB-1995; 95JP-0054977.
PA	(SNOW) SNOW BRAND MILK PROD CO LTD.
XX	
PI	Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PL	Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR	WPI; 1996-402320/40.
NR	N-PSDB; 136685.
XX	
PT	DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT	for bone resorption control, esp. treatment of osteoporosis
XX	
PS	Disclosure; Page 64-66; 183pp; Japanese.
CC	This sequence represents the full length osteoclastogenesis inhibitory
CC	factor (OCIF) of the invention. The OCIF has a molecular weight by
CC	SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-
CC	reducing conditions. The protein is adsorbed onto cation-exchange
CC	resin and its activity is lowered after 10 mins at 70 deg.C., or
CC	30 mins at 56 deg.C., and is lost after 10 mins at 90 deg.C. Or it is
CC	useful in the control of bone resorption and therefore in the
CC	treatment and prevention of disorders of bone resorption, e.g.
CC	osteoporosis.
XX	
SO	Sequence 401 AA;
Query Match	87.8%; Score 977; DB 17; Length 401;
Best Local Similarity	85.2%; Pred.No. 7.5e+93;
Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;	
QY	1 SGNRRATQKCIGIDVTLCLEARFPPRAVPRIIPNLMSLVSDSPGKVVAESVERIKRN...
DB	186 sgnstscitkcgldvlfceatfrfavpekfcpnwslsvdnlpgetkvnaesverikrds... 245
QY	61 SOEGFOFLAKLMKHONROEMWKRIIODIDCESSVOHRHGSHNTTBOALLAMESTL...
DB	246 sqegtfgllklwknqnkqgdvlvkkiqididlcemsqvghnhanltfqlslmesj... 5
QY	121 KISPEIEIRTKTCSSQLLLSLMRINKGDODTLGLMWALKHLKTSHPPKTVTFST...
DB	306 kvgsediekltkackpsdqilklislwlkingdgtlglmhalkhsctylfpkvtcsl... 365
QY	181 RKTMRFLASFMYRLYLQKLFLFMIGNOVQVKISCL 216
DB	366 ktiriflnstcmrykygklflfmignovsqvskscl 401

QY	121	KISEEELIERTKTSSEOLKLSTLRINRGDDTLAKGLMVALKHLSHPRTVTH
Db	306	kvsgeedtektckackpsdqikllslwrlngodotklqgmhalnksklyhnfpkvtrs
QY	181	RKTMRPLHSFTMYRLYOKLEFLEMIGNOVOSVKISCL 216
Db	366	KtIrflhsftemyklygkklflemignvgvskiscl 401
RESULT	10	
ID	Y05742	
XX	Y05742 standard; Protein; 401 AA.	
AC	Y05742;	
XX	19-JUL-1999 (first entry)	
DT	Tumour necrosis factor receptor TR1.	
DE	Tumour necrosis factor receptor; TR1; osteoprotegerin; agonist:	
XX	antagonist; screening; human; cancer; AIDS; Alzheimer's disease;	
KW	inflammation; arthritis; septicemia; autoimmune disease;	
KW	pneumonia; inflammatory bowel disease; transplant rejection;	
KW	graft versus host disease; infection; stroke; ischaemia;	
KW	acute respiratory disease syndrome; restenosis; brain injury;	
KM	bone disease; atherosclerosis; therapy.	
XX		
OS	Homo sapiens.	
PN	EP911633-A1.	
XX	28-APR-1999.	
PD	02-OCT-1998: 98BP-0203332.	
PF	08-OCT-1997: 97US-0061334.	
XX	(SMIR) SMITHKLINE BEECHAM CORP.	
PA	Mcdonnell PC, Young PR, Zou J:	
PI	WPI: 1999-246560/21.	
DR		
XX	Identifying agonists and antagonists of tumor necrosis factor	
PT	related receptors TR1, TR3 and TR5, and of ligand TR3, useful for	
PT	treatment of cancer, AIDS, Alzheimer's disease, bone disease etc	
PS	Disclosure; Page 10-12: 23pp: English.	
XX		
CC	The present sequence represents tumour necrosis factor receptor	
CC	(TNFR) TR1, also known as osteoprotegerin. The invention relat-	
CC	to TNFR related polypeptides TR1, TR3 and TR5 (see Y05742-44) a	
CC	their ligand TR3 (see Y05745). TR1, TR3, TR5 and TR3 are used	
CC	claimed methods of identifying agonists and antagonists, i.e.	
CC	compounds that bind to the receptors or ligand, and which activa-	
CC	(agonist) or inhibit activation of (antagonists) TR1, TR3, TR5	
CC	TR3. A screening kit for identifying agonists, antagonists, li-	
CC	ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or	
CC	TR3 polypeptide is provided. The agonists and antagonists are	
CC	useful for treatment of chronic and acute inflammation, arthritis,	
CC	septicemia, autoimmune disease e.g. inflammatory bowel disease;	
CC	pneumonia, transplant rejection, graft versus host disease,	
CC	infection, stroke, ischaemia, acute respiratory disease syndrome;	
CC	restenosis, brain injury, AIDS, bone diseases, cancer (e.g.	
CC	lymphoproliferative disorders), atherosclerosis and Alzheimer's	
CC	disease, etc., caused by imbalance of TR1, TR3, TR5 or TR3.	
XX		
SQ	Sequence 401 AA:	
Query Match	87.8%; Score 977; DB 20; Length 401;	
Best Local Similarity	85.2%; Pred. No. 7, 5e-93;	

xx	SO	Sequence	401 AA:	
		Query Match	87.8%; Score 977;	DB 20; Length 401;
		Best Local Similarity	85.2%; Pred. No. 7.5e-93;	
		Matches 184;	Conservative 19;	Mismatches 13; Indels 0;
OY		1	SGNREATOKCGIDVWLCBEAFEPFVAPPTKIIPNMTSLVYDSLPGTRKVNASEVERIKRKT	100
DB		186	sgnsstctkcgjdvcllceaeffrfavpctkfpnwslyvndnlpqtkvnaesverikrghs	245
OY		61	SOEOTFOLLKMKHONRDOENWKTTIODIDCESSVORHGHSNLTTEOLLAMESLPKX	120
DB		246	sqegftqllklwkbqnpqgdvkvkllqgdldlensvgrhignanltfegrlreslmslpkx	405
OY		121	KISPEIRTRTRCTKSSOLLKLLSLMRKKNODOTLNGMLMALHLKTSHPKTYTHSI	180
DB		306	kygaediecltlackpsdqllkliswlrkngddcllygmlhalhsktlyhnpkvtgs	365
OY		181	RKTMRFLLHSFTWYRLYOKLFLFMIGNOVOSVKISCL	216
DB		366	ktlrlfnstfmyklyqkllflemignqvsvklscl	401
RESULT		12		
ID		W83926	standard; Protein;	401 AA.
AC		W83926;		
XX		01-MAR-1999	(first entry)	
XX		Human FTHMA-070 protein.		
DE				
XX		FTHMA-070; human; neurological disorder; therapy; diagnosis.		
KW		Homo sapiens.		
XX				
OS		Homo sapiens.		
XX				
FT		Key	Location/Qualifiers	
FT		Peptide	1..21	
FT		Protein	/label= Sig-peptide	
FT			22..401	
FT			/label= Mat_protein	
XX				
PN		W09848051-A2.		
XX				
PD		29-OCT-1998.		
XX				
PE		17-APR-1998;	98WO-US07714.	
XX				
PR		10-OCT-1997;	97US-0062017.	
PR		18-APR-1997;	97US-0044746.	
PA		(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.		
XX				
PI		Holtzman D, McCarthy SA;		
XX				
DR		WPI: 1999-024021/02.		
XX		N-PSDB: V69277.		
XX				
PT		New isolated human FTHMA-070 and T85 proteins - used to develop		
PT		products for the diagnosis and therapy of disorders involving		
PT		cellular processes, e.g. neuronal development.		
XX				
PS		Claim 8; Fig 1; 127bp; English.		
CC		This is the amino acid sequence of human FTHMA-070, a novel protein		
CC		having homology to tumour necrosis factor receptor. The sequence		
CC		was deduced from that of a cDNA clone (see V69277) isolated from a		
CC		cardiac coronary artery smooth muscle cell library. FTHMA-070		
CC		nucleic acids and polypeptides of the invention are useful as		
CC		modulating agents in regulating a variety of cellular processes.		

CC They can be used for identifying compounds which bind to or modulate
 CC the activity of the polypeptides (claimed). They can also be used
 CC in screening assays, detection assays (e.g. chromosomal mapping,
 CC tissue typing, forensic biology), predictive medicine (e.g.
 CC diagnostic assays, prognostic assays, monitoring clinical trials,
 CC and pharmacogenomics), and methods of treatment (e.g. therapeutic
 CC and prophylactic) e.g. for neurological disorders.

XX Sequence 401 AA;

SO Query Match 87.8%; Score 977; DB 20: Length 401;

Best Local Similarity 85.2%; Pred. No. 7.5e-93;

Matches 184; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 SGNREATOKGIDVTLCCEAFRRFVPTKTIIPNMLSVYVDSLPGTKVAESVERIKRRHS 60

DB 186 sgnsestqcgldvtlceeafrfayptkfpnwlsvlvdnlpqtkvaesverikrrhs 245

QY 61 SOEOTFOLLKMKHONRDOEWKRIIDIDICSSVORHGHSLTTEOLALMESLPK 120

DB 246 sgeqlfqlklwkhqkqgdvkvkldidicnsygrhghantlfeqlrlsmeslpk 305

QY 121 KISPEIERTKRTCKSSQQLKLSLWIRKNGDDDTLKGMLYALKHLKTSHPKTVTSL 180

DB 306 kvgaedlektlkackpsdqllkllslwlrkngddtlkgmlhalkhsktyhfpkvtqsl 365

QY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216

DB 366 ktirflhsftmyrlyqklflemignqvsvkiscsl 401

RESULT 13

R99937 R99937 standard; Protein; 359 AA.

XX AC R99937;

DT 23-APR-1997 (first entry)

XX DE Mutated OCIF, OCIF-DCR2.

XX KW Osteoclastogenesis inhibitory factor; OCIF, heparin; bone resorption;

XX KM osteoporosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "Signal peptide"

FT Misc-difference 63..64 /note= "Mature OCIF-DCR2"

XX /note= "Position of deletion, delta 43-84"

XX MO9626217-A1.

XX PD 29-AUG-1996.

XX PF 20-FEB-1996; 96WO-JP00374.

XX PR 21-JUL-1995; 95JP-0207508.

XX PR 20-FEB-1995; 95JP-0054977.

XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;

XX PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

XX DR WPI; 1996-402320/40.

XX DR N-PSDB; T33167.

PT DNA encoding osteoclastogenesis inhibitory factor protein - useful

PT for bone resorption control, esp. treatment of osteoporosis

XX PS Claim 47; Page 107-109; 183pp; Japanese.

XX CC This sequence represents a mutated version of the full length

CC osteoclastogenesis inhibitory factor (OCIF) of the invention.

CC sequence represents OCIF-DCR2 in which amino acids 43-84 of the

CC mature OCIF protein are deleted. The OCIF of the invention

CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions

CC and 120 kD under non-reducing conditions. The protein is adsorbed into

CC cation-exchangers or heparin and its activity is lowered after 10 mins

CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70

CC deg.C. OCIF is useful in the control of bone resorption and the score

CC in the treatment and prevention of disorders of bone resorption, e.g.

XX osteoporosis.

SO Sequence 359 AA;

Query Match 87.3%; Score 972; DB 17: Length 359;

Best Local Similarity 84.7%; Pred. No. 2.1e-92;

Matches 183; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 SGNREATOKGIDVTLCCEAFRRFVPTKTIIPNMLSVYVDSLPGTKVAESVERIKRRHS 60

DB 144 sgnsestqcgldvtlceeafrfayptkfpnwlsvlvdnlpqtkvaesverikrrhs 203

QY 61 SOEOTFOLLKMKHONRDOEWKRIIDIDICSSVORHGHSLTTEOLALMESLPK 120

DB 204 sgeqlfqlklwkhqkqgdvkvkldidicnsygrhghantlfeqlrlsmeslpk 263

QY 121 KISPEIERTKRTCKSSQQLKLSLWIRKNGDDDTLKGMLYALKHLKTSHPKTVTSL 180

DB 264 kvgaedlektlkackpsdqllkllslwlrkngddtlkgmlhalkhsktyhfpkvtqsl 323

QY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216

DB 324 ktirflhsftmyrlyqklflemignqvsvkiscsl 359

RESULT 14

W57635 W57635 standard; Protein; 401 AA.

XX AC W57635;

DT 27-AUG-1998 (first entry)

XX DE TR1 receptor protein.

XX DE TR1 receptor protein.

XX TR1 receptor: tumour necrosis factor receptor-1; TNF-alpha; TNF-1; a;

XX inhibitor; tumour growth; tumour necrosis; microorganism infection;

XX cellular differentiation stimulation; ionising radiation; septic shock;

XX anti-viral response; growth regulator; immune response; meningococemia;

XX autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria;

XX AIDS; therapy.

XX OS Homo sapiens.

XX PN WO9812344-A1.

XX PD 26-MAR-1998.

XX PF 18-SEP-1996; 96WO-US15003.

XX PR 18-SEP-1996; 96WO-US15003.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Fleischmann RD, Greene JM, Ni J;

XX DR WPI; 1998-217278/19.

XX DR N-PSDB; V24486.

XX New isolated tumour necrosis factor receptor - useful for developing
 PT products for treating, e.g. tumours, auto-immune disease(s), graft
 PR rejection, apoptosis or inflammation
 PS
 XX

Claim 13; Fig 1; 111pp; English.

CC This sequence is a tumour necrosis factor receptor-1 (TR1) receptor
 CC of the invention. The DNA can be used to produce a recombinant host
 CC cell by inserting it into a vector, which is then used to transfect the
 CC host cell. The TR1 receptor can bind both TNF-alpha and TNF-beta. TR1
 CC receptor agonists can be used for inhibition of tumour growth and
 CC necrosis of tumours. They can also be used to stimulate cellular
 CC differentiation, e.g. T cell, fibroblasts or hematopoietic cell
 CC against microorganisms and prevent related disease. The agonists may
 CC also be used to protect against the deleterious effects of ionising
 CC radiation produced during a course of radiotherapy, e.g. denaturation of
 CC enzymes, lipid peroxidation or DNA damage. The agonists may further be
 CC used to mediate an anti-viral response, to regulate growth, to mediate
 CC the immune response and to treat immunodeficiencies related to diseases
 CC such as HIV. Antagonists to the TR1 receptor may be used to treat
 CC autoimmune diseases, e.g. graft versus host rejection and allograft
 CC rejection, and T cell mediated autoimmune diseases. They may also be used
 CC to prevent apoptosis. They may also be used to prevent cytotoxicity and
 CC to treat septic shock, meningococemia, inflammation, bacterial
 CC infections, cachexia, cerebral malaria or AIDS. The products can also be
 CC used for diagnosing the above diseases.
 CC
 XX

Sequence 401 AA:

Query Match 87.3%; Score 972; DB 19; Length 401;
 Best Local Similarity 84.7%; Pred. No. 2,5e-92;
 Matches 183; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 SCNRATQKCGIDVTLCEAFRFAVPTKIPNMLSVLYDSLPGRKVAESVERIKRRHS 60
 DB 166 sgnsetqkcgldvltlceaftrfapvptkfpnwslvldnlpgrkvaesverikrrhs 245
 OY 61 SOEQFOLKLKMKHNRDQEMWKIIODIDCESSQVRHLGHSNLTTEQLALMESLPCK 120
 DB 246 sqeqfqlklkhwkqkqdkvkkidldcensvgrhghantlftqslrslmeslpck 305
 OY 121 KISPEIERTRKTCSSSEQLKLSLMRIKNGDODTLKGLMALKHLKTSHPKTVTHSI 180
 DB 306 kvgaediektlkackpsdqilklislrwknqgdqtlkglmalhsktshpklvtqsl 365
 OY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216
 DB 366 kktirflhsftmyklykrlflemignqvsvkiscsl 401

RESULT 15
 ID W38345 standard; Protein; 401 AA.
 XX
 AC W38345;
 XX

DT 20-APR-1998 (first entry)
 XX
 DE Human osteoprotegerin.

KM Osteoprotegerin; antibody; diagnosis; affinity purification;
 KM recombinant production; transgenic animal; treatment; prevention;
 KM antisense oligonucleotide; probe; detection; screening; human;
 KM bone disease; osteoporosis; Paget's disease; hypercalcaemia;
 KM hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
 KM osteolytic metastasis; periodontal bone loss; bone necrosis;
 KM osteopenia.
 XX
 OS Homo sapiens.
 XX

PN DE19654610-A1.

XX 26-JUN-1997.

XX 20-DEC-1996; 96DE-1054610.

XX 03-SEP-1996; 96US-0706945.

XX 22-DEC-1995; 95US-0577788.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Calzone FJ, Lacey DL, Chang NS.

XX WPI; 1997-334271/31.

XX N-PSDB; T96063.

XX Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis
 PS

Claim 23; Pages 109-111; 182pp; German.

CC The present sequence is human osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express
 CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopenia.
 CC
 XX

Sequence 401 AA:

Query Match 87.1%; Score 969; DB 18; Length 401;
 Best Local Similarity 84.7%; Pred. No. 5e-92;
 Matches 183; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 SCNRATQKCGIDVTLCEAFRFAVPTKIPNMLSVLYDSLPGRKVAESVERIKRRHS 60
 DB 166 sgnsetqkcgldvltlceaftrfapvptkfpnwslvldnlpgrkvaesverikrrhs 45
 OY 61 SOEQFOLKLKMKHNRDQEMWKIIODIDCESSQVRHLGHSNLTTEQLALMESLPCK 120
 DB 246 sqeqfqlklkhwkqkqdkvkkidldcensvgrhghantlftqslrslmeslpck 305
 OY 121 KISPEIERTRKTCSSSEQLKLSLMRIKNGDODTLKGLMALKHLKTSHPKTVTHSI 180
 DB 306 kvgaediektlkackpsdqilklislrwknqgdqtlkglmalhsktshpklvtqsl 365
 OY 181 RKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 216
 DB 366 kktirflhsftmyklykrlflemignqvsvkiscsl 401

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